

## Human DNase I

LOCUS HUMDNASEI 1039 bp mRNA PRI 06-MAR-1995  
 DEFINITION Human DNase I mRNA, complete cds.  
 ACCESSION M55983  
 VERSION M55983.1 GI:181623  
 KEYWORDS DNase I.  
 SOURCE Human pancreas, cDNA to mRNA.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1039)  
 AUTHORS Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L.  
 TITLE Recombinant human DNase I reduces the viscosity of cystic fibrosis  
 sputum  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)  
 MEDLINE 91067672  
 FEATURES Location/Qualifiers  
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             VEVMLK"  
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     mat peptide 226..1005  
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                   /product="DNase I"  
 BASE COUNT 226 a 305 c 282 g 226 t  
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     61 tttttcttta gcagcaaaag gagaaaattg tcatcaaagg atattccaga ttcttgacag  
     121 cattctcgtc atctctgagg acatcaccat catctcagga tgaggggcat gaagctgctg  
     181 ggggcgctgc tggcactggc ggccctactg caggggggccc tgtccctgaa gatcgcagcc  
     241 ttcaacatcc agacatttgg ggagaccaag atgtccaatg ccaccctcgt cagctacatt  
     301 gtgcagatcc tgagccgcta tgacatcgcc ctggtccagg aggtcagaga cagccacctg  
     361 actgccgtgg ggaagctgct ggacaacctc aatcaggatg caccagacac ctatcactac  
     421 gtggtcagtg agccactggg acggaacagc tataaggagc gctacctgtt cgtgtacagg  
     481 cctgaccagg tgtctgcggt ggacagctac tactacgatg atggctgcga gccctgcggg  
     541 aacgacacct tcaaccgaga gccagccatt gtcaggttct tctcccgtt cacagaggtc  
     601 agggagtttg ccattgttcc cctgcatgcg gccccggggg acgcagtagc cgagatcgac  
     661 gctctctatg acgtctacct ggatgtccaa gagaaatggg gcttggagga cgtcatgttg  
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     781 ctgtggacaa gccccacctt ccagtggctg atccccgaca gcgctgacac cacagctaca  
     841 cccacgcact gtgcctatga caggatcgtg gttgcaggga tgctgctccg aggcgcggtt  
     901 gttcccgact cggtcttctc ctttaacttc caggctgcct atggcctgag tgaccaactg  
     961 gcccaagcca tcagtgacca ctatccagtg gaggtgatgc tgaagtgagc agcccctccc  
     1021 cacaccagtt gaactgcag

//

**Fig. 1**

## Human DNase I construct

LOCUS MHDNASE.DN 783 bp mRNA PRI 06-MAR-1995  
 DEFINITION Human DNase I mRNA, complete cds, Mature sequence modified to remove NarI site  
 ACCESSION M55983  
 NID g181623  
 KEYWORDS DNase I.  
 SOURCE Human pancreus, cDNA to mRNA.  
 ORGANISM Homo sapiens  
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1039)  
 AUTHORS Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.  
 TITLE Recombinant human DNase I reduces the viscosity of cystic fibrosis sputum  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)  
 MEDLINE 91067672  
 FEATURES Location/Qualifiers  
 source 1..1039  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="hDNase-18-1"  
 /tissue\_type="pancreas"  
 sig\_peptide 160..225  
 /gene="DNase I"  
 CDS 160..1008  
 /gene="DNase I"  
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 /product="DNase I"  
 /db\_xref="PID:g181624"  
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 PCGNDTFNREPAIVRFFSRFTEVREFAIVPLHAAPGDAVAEIDALYDVYLDVQEKWGL  
 EDVMLMGDFNAGCSYVRPSQWSSIRLWTSPTFQWLIPDSADTTATPTPHCAYDRIVVAG  
 MLLRGAVVPDSALPFNFQAAAYGLSDQLAQAI SDHYPVEVMLK"  
 gene 160..1008  
 /gene="DNase I"  
 mat\_peptide 226..1005  
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 BASE COUNT 168 a 236 c 220 g 159 t  
 ORIGIN

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1 CTGAAGATCG CAGCCTTCAA CATCCAGACA TTTGGGGAGA CCAAGATGTC CAATGCCACC
61 CTCGTCAGCT ACATTGTGCA GATCCTGAGC CGCTACGACA TCGCCCTGGT CCAGGAGGTC
121 AGAGACAGCC ACCTGACTGC CGTGGGGAAG CTGCTGGACA ACCTCAATCA GGACGCACCA
181 GACACCTATC ACTACGTGGT CAGTGAGCCA CTGGGACGGA ACAGCTATAA GGAGCGCTAC
241 CTGTTCTGTG ACAGGCCTGA CCAGGTGTCT GCGGTGGACA GCTACTACTA CGATGATGGC
301 TGCGAGCCCT GCGGGAACGA CACCTTCAAC CGAGAGCCAG CCATTGTCAG GTTCTTCTCC
361 CGGTTACAG AGGTCAGGGA GTTTGCCATT GTTCCCCTGC ATGCGGCCCC GGGGACGCA
421 GTAGCCGAGA TCGACGCTCT CTATGACGTC TACCTGGATG TCCAAGAGAA ATGGGGCTTG
481 GAGGACGTCA TGTTGATGGG CGACTTCAAT GCGGGCTGCA GCTATGTGAG ACCCTCCCAG
541 TGGTCAATCCA TCCGCCTGTG GACAAGCCCC ACCTTCCAGT GGCTGATCCC CGACAGCGCT
601 GACACCACAG CTACACCCAC GCACTGTGCC TATGACAGGA TCGTGTTGTC AGGGATGCTG
661 CTCCGAGGGG CCGTTGTTCC CGACTCGGCT CTTCCCTTTA ACTTCCAGGC TGCCTATGGC
721 CTGAGTGACC AACTGGCCCA AGCCATCAGT GACCACTATC CAGTGAGGAT GATGCTGAAG
781 TGA
  
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*Fig. 2(A)*

LOCUS PAS155\_GB. 858 BP SS-DNA SYN 29-AUG-2000  
 DEFINITION -  
 ACCESSION -  
 KEYWORDS -  
 SOURCE -

FEATURES Location/Qualifiers  
 frag 10..75  
 /note="160 to 225 of Untitled1"  
 frag <10..>75  
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 source <10..>75  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="hDNase-18-1"  
 /tissue\_type="pancreas [Split]"  
 sig\_peptide 10..75  
 /gene="DNase I"  
 CDS 10..>75  
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 /codon\_start="1"  
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 /db\_xref="PID:g181624"

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LFVYRPDQVSAVDSYYDDGCEPCGNDTFNREPAIVRFFSRFTEVREFAIVPLHAAPG

D... [Split]"  
 gene 10..>75  
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 frag 76..858  
 /note="1 to 783 of mod humanDNaseI"  
 frag 76..858  
 /note="1 to 72 of 104linker"  
 frag join(76..>129,<131..147)  
 /note="1 to 72 of 103linker [Split]"  
 frag join(76..>126,<127..>129,<131..147)  
 /note="1 to 78 of 102linker [Split]"

BASE COUNT 177 A 260 C 251 G 170 T 0 OTHER

ORIGIN -

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1  GCGGCCACCA TGAGGGGCGAT GAAGCTGCTG GGGGCGCTGC TGGCACTGGC GGCCCTACTG
61 CAGGGGGGCCG TGTCCCTGAA GATCGCAGCC TTCAACATCC AGACATTTGG GGAGACCAAG
121 ATGTCCAATG CCACCCTCGT CAGCTACATT GTGCAGATCC TGAGCCGCTA CGACATCGCC
181 CTGGTCCAGG AGGTCAGAGA CAGCCACCTG ACTGCCGTGG GGAAGCTGCT GGACAACCTC
241 AATCAGGACG CACCAGACAC CTATCACTAC GTGGTCAGTG AGCCACTGGG ACGGAACAGC
301 TATAAGGAGC GCTACCTGTT CGTGACAGG CCTGACCAGG TGTCTGCGGT GGACAGCTAC
361 TACTACGATG ATGGCTGCGA GCCCTGCGGG AACGACACCT TCAACCGAGA GCCAGCCATT
421 GTCAGGTTCT TCTCCCGGTT CACAGAGGTC AGGGAGTTTG CCATTGTTCC CCTGCATGCG
481 GCCCCGGGGG ACGCAGTAGC CGAGATCGAC GCTCTCTATG ACGTCTACCT GGATGTCCAA
541 GAGAAATGGG GCTTGGAGGA CGTCATGTTG ATGGGCGACT TCAATGCGGG CTGCAGCTAT
601 GTGAGACCCT CCCAGTGGTC ATCCATCCGC CTGTGGACAA GCCCCACCTT CCAGTGGCTG
661 ATCCCCGACA GCGCTGACAC CACAGCTACA CCCACGCACT GTGCCTATGA CAGGATCGTG
721 GTTGCAGGGA TGCTGCTCCG AGGGGCCGTT GTTCCCGACT CGGCTCTTCC CTTTAACTTC
781 CAGGCTGCCT ATGGCCTGAG TGACCAACTG GCCCAAGCCA TCAGTGACCA CTATCCAGTG
841 GAGGTGATGC TGAAGTGA

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**Fig. 2(B)**

## pAS6 – light chain

LOCUS HMFG1LC2.D 721 bp DNA 18-AUG-1998  
 DEFINITION HUMANISED HMFG1 LIGHT CHAIN Vnp LEADER.  
 ACCESSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 REFERENCE 1 (BASES 1 TO 342)  
 AUTHORS VERHOEYEN ET AL  
 TITLE CONSTRUCTION OF RESHAPED HMFG1 ETC  
 JOURNAL IMMUNOL. (1993):78, 364-370  
 COMMENT SCANNED IN FROM JOURNAL  
 FEATURES  
 SITES

This is the sequence of the HMFG1 light chain gene with the  
 Vnp leader sequence attached. Translate from  
 residue 1. Note residue 399 is T > A in all clones leading  
 to R133 silent mutation (T in Verhoeyen paper)

BASE COUNT 197 a 202 c 182 g 140 t  
 ORIGIN ?

	LEADER SEQ						
1	ATGGGATGGA	GCTGTATCAT	CCTCTTCTTG	GTAGCAACAG	CTACAGGTGT	CCACTCGAC	
61	ATCCAGATGA	CCCAGAGCCC	AAGCAGCCTG	AGCGCCAGCG	TGGGTGACAG	AGTGACCATC	
121	ACCTGTAAGT	CCAGTCAGAG	CCTTTTATAT	AGTAGCAATC	AAAAGATCTA	CTTGGCCTGG	
181	TACCAGCAGA	AGCCAGGTAA	GGCTCCAAAG	CTGCTGATCT	ACTGGGCATC	CACTAGGGAA	
241	TCTGGTGTGC	CAAGCAGATT	CAGCGGTAGC	GGTAGCGGTA	CCGACTTCAC	CTTCACCATC	
301	AGCAGCCTCC	AGCCAGAGGA	CATCGCCACC	TACTACTGCC	AGCAATATTA	TAGATATCCT	
361	CGGACGTTTC	GCCAAGGGAC	CAAGGTGGAA	ATCAAACGAA	CTGTGGCTGC	ACCATCTGTC	
421	TTCATCTTCC	CGCCATCTGA	TGAGCAGTTG	AAATCTGGAA	CTGCCTCTGT	TGTGTGCCTG	
481	CTGAATAACT	TCTATCCCAG	AGAGGCCAAA	GTACAGTGGA	AGGTGGATAA	CGCCCTCCAA	
541	TCGGGTAAC	CCCAGGAGAG	TGTCACAGAG	CAGGACAGCA	AGGACAGCAC	CTACAGCCTC	
601	AGCAGCACCC	TGACGCTGAG	CAAAGCAGAC	TACGAGAAAC	ACAAAGTCTA	CGCCTGCGAA	
661	GTCACCCATC	AGGGCCTGAG	CTCGCCCGTC	ACAAAGAGCT	TCAACAGGGG	AGAGTGTTAG	
721	A						

//

**Fig. 3(A)**

LOCUS HHMFG1KLC\_ 730 BP SS-DNA SYN 29-AUG-2000

DEFINITION -

ACCESSION -

KEYWORDS -

SOURCE -

FEATURES

Location/Qualifiers

frag 10..730

/note="1 to 721 of hHMFG1light chain"

frag 10..730

/note="1 to 72 of 104linker"

frag join(10..>63,<65..81)

/note="1 to 72 of 103linker [Split]"

frag join(10..>60,<61..>63,<65..81)

/note="1 to 78 of 102linker [Split]"

BASE COUNT 198 A 208 C 184 G 140 T 0 OTHER

ORIGIN -

1 GCCGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTGTC

61 CACTCCGACA TCCAGATGAC CCAGAGCCCA AGCAGCCTGA GCGCCAGCGT GGGTGACAGA

121 GTGACCATCA CCTGTAAGTC CAGTCAGAGC CTTTTATATA GTAGCAATCA AAAGATCTAC

181 TTGGCCTGGT ACCAGCAGAA GCCAGGTAAG GCTCCAAAGC TGCTGATCTA CTGGGCATCC

241 ACTAGGGAAT CTGGTGTGCC AAGCAGATTC AGCGGTAGCG GTAGCGGTAC CGACTTCACC

301 TTCACCATCA GCAGCCTCCA GCCAGAGGAC ATCGCCACCT ACTACTGCCA GCAATATTAT

361 AGATATCCTC GGACGTTTCGG CCAAGGGACC AAGGTGGAAA TCAAACGAAC TGTGGCTGCA

421 CCATCTGTCT TCATCTTCCC GCCATCTGAT GAGCAGTTGA AATCTGGAAC TGCCTCTGTT

481 GTGTGCCTGC TGAATAACTT CTATCCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC

541 GCCCTCCAAT CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA GGACAGCACC

601 TACAGCCTCA GCAGCACCCT GACGCTGAGC AAAGCAGACT ACGAGAAACA CAAAGTCTAC

661 GCCTGCGAAG TCACCCATCA GGGCCTGAGC TCGCCCGTCA CAAAGAGCTT CAACAGGGGA

721 GAGTGTTAGA

//

***Fig. 3(B)***

**HMFG-1 light chain with Vnp Leader (shaded)**

MGWSCILFLVATATGVHSDIQMTQSPSSLSASVGDRVTITCKSSQSL  
LYSSNQKIYLA WYQQKPGKAPKLLIWASTRESGVPSRFSGSGSGT  
DFTFTISLQPEDIATYYCQQYYRYPRTFGQGTKVEIKRTVAAPSVFI  
FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESV  
TEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN  
RGEC

***Fig. 3(C)***

## pAS6 – heavy chain

LOCUS HHMFG1HC.D 1404 bp DNA 14-AUG-1998  
 DEFINITION HUMANISED HMFG1 heavy chain  
 ACCESSION HHMFG1H  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 REFERENCE  
 AUTHORS VERHOEYEN ET AL  
 TITLE CONSTRUCTION OF RESHAPED HMFG1 etc  
 JOURNAL IMMUNOL. (1993):78, 364-370  
 COMMENT VH domain SCANNED IN FROM JOURNAL  
 FEATURES AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A)  
 FEATURES Residue 963 is G > T leading to silent mutation in all clones  
 SITES Note  
 BASE COUNT 333 a 439 c 379 g 253 t  
 ORIGIN ?

LEADER

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1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATAACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTG GTGGAACCTA
541 GCGGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAACTC ACACATGCCC ACCGTGCCCA GCACCTGAAc TCCTGGGGGG ACCGTCAGTC
781 TTCCTCTTCC CCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA
841 TGCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC
901 GCGGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC
961 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG
1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA
1081 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG
1141 AACCAGGTCA GCCTGACCTG CCTGGTCAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG
1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC
1261 GACGGCTCCT TCTTCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG
1321 AACGTCTTCT CATGCTCCGT GATGATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC
1381 CTCTCCCTGT CTCCGGGTAA ATGA
  
```

Antibody DNase Fusions Made Here  
(eg pAS34----39.)

End of lower hinge region of heavy chain. PAPE Amino  
Acid Seq. Fab'<sub>2</sub> fusions were made at this point.

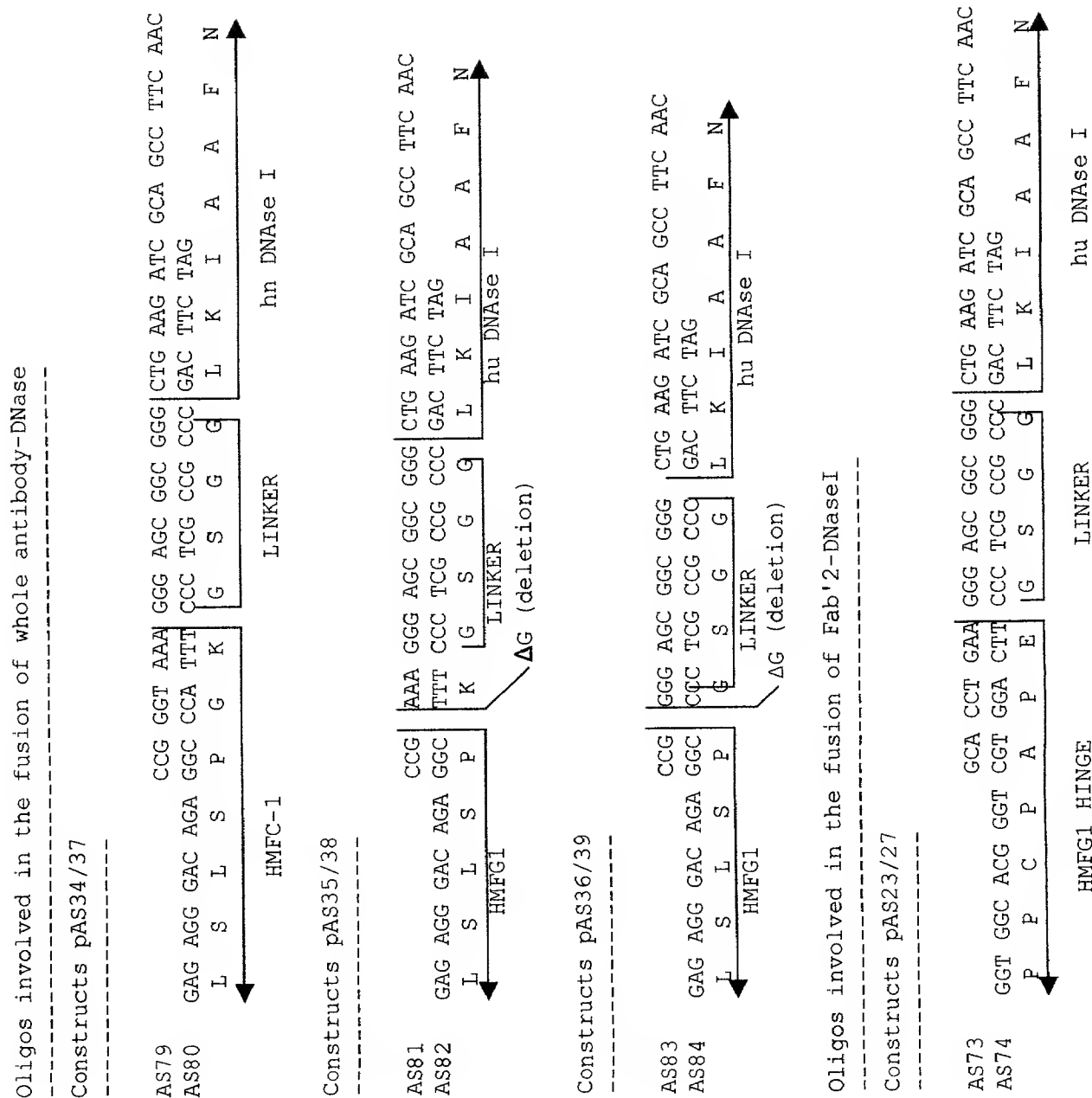
Those with HYBRID HINGES are altered further  
up i.e.

This part GACAAAAC TGACACA  
D K T H T

After this sequence you get the HYBRID HINGE + LINKER SEQUENCES  
Then DNase I (eg Fab-DNase construct pAS302)

**Fig. 3(D)**

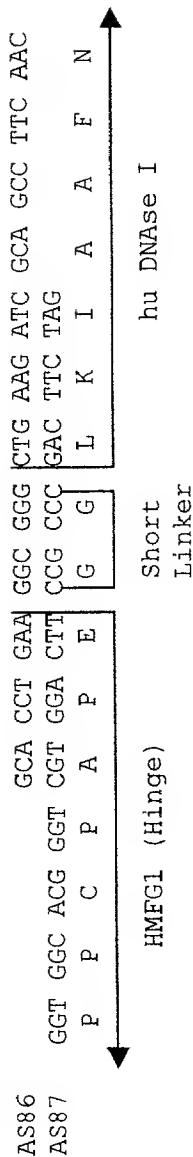
Fig. 4(A)



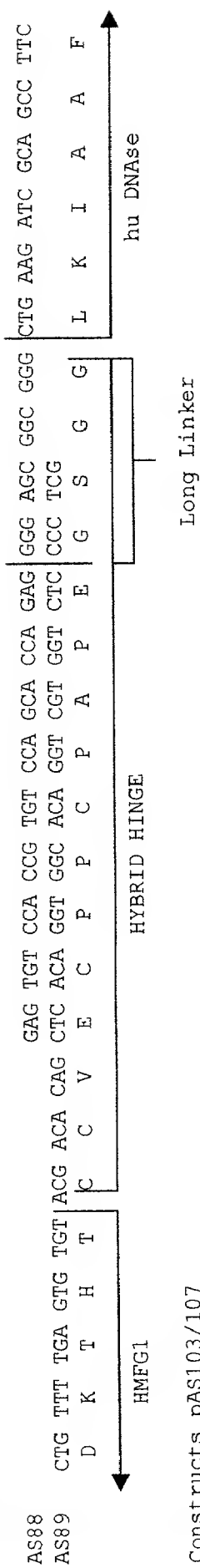


Oligos involved in the fusion of new Fab'2-DNaseI molecules (5.7.99)

Constructs pAS101/105



Constructs pAS102/106



Constructs pAS103/107

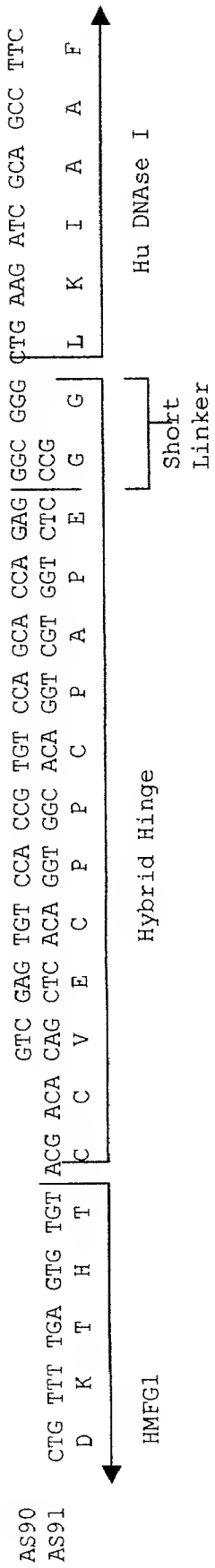


Fig. 4(B)

## pAS23

LOCUS PAS23.DNA 1554 bp mRNA PRI 06-MAR-1995  
DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I (construct 1)  
ACCESSION  
NID  
KEYWORDS DNase I.  
SOURCE DNase I sequence is from assembled oligos (thus modified c/f  
MHDNASE1.dna)  
ORGANISM Homo sapiens  
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;  
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.  
TITLE Recombinant human DNase I reduces the viscosity of cystic  
fibrosis  
JOURNAL sputum  
Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)  
MEDLINE 91067672  
BASE COUNT 344 a 468 c 434 g 308 t  
ORIGIN

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1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCAAGTCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAAGTCA
541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAATC ACACATGCCC ACCGTGCCCC GCACCTGAAG GGAGCGGCGG GCTGAAGATC
781 GCAGCCTTCA ACATCCAGAC ATTTGGGGAG ACCAAGATGT CCAATGCCAC CCTCGTCAGC
841 TACATTGTGC AGATCCTGAG CCGCTACGAC ATCGCCCTGG TCCAGGAGGT CAGAGACAGC
901 CACCTGACTG CCGTGGGGAA GCTGCTGGAC AACCTCAATC AGGACGCACC AGACACCTAT
961 CACTACGTGG TCAGTGAGCC ACTGGGACGG AACAGCTATA AGGAGCGCTA CCTGTTCTGT
1021 TACAGGCCTG ACCAGGTGTC TGCGGTGGAC AGCTACTACT ACGATGATGG CTGCGAGCCC
1081 TGCGGGAACG ACACCTTCAA CCGAGAGCCA GCCATTGTCA GGTCTTCTC CCGGTTTACA
1141 GAGGTCAGGG AGTTTGCCAT TGTTCCCCTG CATGCGGCCC CGGGGGACGC AGTAGCCGAG
1201 ATCGACGCTC TCTATGACGT CTACCTGGAT GTCCAAGAGA AATGGGGCTT GGAGGACGTC
1261 ATGTTGATGG GCGACTTCAA TGCGGGCTGC AGCTATGTGA GACCCTCCA GTGGTCATCC
1321 ATCCGCCTGT GGACAAGCCC CACCTTCCAG TGGCTGATCC CCGACAGCGC TGACACCACA
1381 GCTACACCCA CGCACTGTGC CTATGACAGG ATCGTGTTG CAGGGATGCT GCTCCGAGGG
1441 GCCGTTGTTT CCGACTCGGC TCTTCCCTTT AACTTCCAGG CTGCCTATGG CCTGAGTGAC
1501 CAACTGGCCC AAGCCATCAG TGACCACTAT CCAGTGGAGG TGATGCTGAA GTGA
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**Fig. 5(A)**

LOCUS FDDNASE23\_ 1554 BP SS-DNA SYN 25-AUG-2000  
 DEFINITION -  
 ACCESSION -  
 KEYWORDS -  
 SOURCE -

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 /note="1 to 66 of 23/27linker"  
 frag join(721..>735,<736..786)  
 /note="1 to 78 of 102linker [Split]"

BASE COUNT 344 A 466 C 435 G 309 T 0 OTHER  
 ORIGIN -

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG  
 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC  
 121 TGCAAGGCTT CTGGCTACAC CTTCAAGTGC TACTGGATAG AGTGGGTGCG CCAGGCTCCA  
 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATAACAAT  
 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG  
 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC  
 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC  
 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG  
 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA  
 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC  
 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC  
 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT  
 721 GACAAAACTC ACACATGTCC ACCGTGTCCA GCACCAGAGG GGAGCGGCGG GCTGAAGATC  
 781 GCAGCCTTCA ACATCCAGAC ATTTGGGGAG ACCAAGATGT CCAATGCCAC CCTCGTCAGC  
 841 TACATTGTGC AGATCCTGAG CCGCTACGAC ATCGCCCTGG TCCAGGAGGT CAGAGACAGC  
 901 CACCTGACTG CCGTGGGGAA GCTGCTGGAC AACCTCAATC AGGACGCACC AGACACCTAT  
 961 CACTACGTGG TCAGTGAGCC ACTGGGACGG AACAGCTATA AGGAGCGCTA CCTGTTCTGTG  
 1021 TACAGGCCTG ACCAGGTGTC TGCGGTGGAC AGCTACTACT ACGATGATGG CTGCGAGCCC  
 1081 TGCGGGAACG ACACCTTCAA CCGAGAGCCA GCCATTGTCA GGTTCCTTCTC CCGGTTTACA  
 1141 GAGGTCAGGG AGTTTGCCAT TGTTCCCCTG CATGCGGCCC CGGGGGACGC AGTAGCCGAG  
 1201 ATCGACGCTC TCTATGACGT CTACCTGGAT GTCCAAGAGA AATGGGGCTT GGAGGACGTC  
 1261 ATGTTGATGG GCGACTTCAA TGCGGGCTGC AGCTATGTGA GACCTCCCA GTGGTCATCC  
 1321 ATCCGCTGT GGACAAGCCC CACCTTCCAG TGGCTGATCC CCGACAGCGC TGACACCACA  
 1381 GCTACACCCA CGCACTGTGC CTATGACAGG ATCGTGGTTG CAGGGATGCT GCTCCGAGGG  
 1441 GCCGTTGTTT CCGACTCGGC TCTTCCCTTT AACTTCCAGG CTGCCTATGG CCTGAGTGAC  
 1501 CAACTGGCCC AAGCCATCAG TGACCACTAT CCAGTGGAGG TGATGCTGAA GTGA

//

**Fig. 5(B)**

```

LOCUS      FDDNASE23K   1563 BP SS-DNA                      SYN      29-AUG-2000
DEFINITION -
ACCESSION  -
KEYWORDS   -
SOURCE     -
FEATURES   Location/Qualifiers
            frag        10..1563
                        /note="1 to 1554 of FdDNase23correct"
            frag        join(10..>729,<796..1563)
                        /note="1 to 1554 of 23.dna [Split]"
            frag        730..795
                        /note="1 to 66 of 23/27linker"
            frag        join(730..>744,<745..795)
                        /note="1 to 78 of 102linker [Split]"
BASE COUNT      345 A      472 C      437 G      309 T      0 OTHER
ORIGIN         -
1  GCCGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTGTC
61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG
121 AAGGTGTCCT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC
181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATTT TACCTGGAAG TAATAATTCT
241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA
361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA
421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCCT CCTCCAAGAG CACCTCTGGG
481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACC GGGTGTCG
541 TGGAAGTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA
601 GGAAGTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC
661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC
721 AAATCTTGTG AAAAACTCA CACATGTCCA CCGTGTCCAG CACCAGAGGG GAGCGGCGGG
781 CTGAAGATCG CAGCCTTCAA CATCCAGACA TTTGGGGAGA CCAAGATGTC CAATGCCACC
841 CTCGTCAGCT ACATTGTGCA GATCCTGAGC CGCTACGACA TCGCCCTGGT CCAGGAGGTC
901 AGAGACAGCC ACCTGACTGC CGTGGGGAAG CTGCTGGACA ACCTCAATCA GGACGCACCA
961 GACACCTATC ACTACGTGGT CAGTGAGCCA CTGGGACGGA ACAGCTATAA GGAGCGCTAC
1021 CTGTTTCGTGT ACAGGCCCTGA CCAGGTGTCT GCGGTGGACA GCTACTACTA CGATGATGGC
1081 TGCAGAGCCCT GCGGGAACGA CACCTTCAAC CGAGAGCCAG CCATTGTCAG GTTCTTCTCC
1141 CGGTTACAG AGGTCAGGGA GTTTGCCATT GTTCCCCTGC ATGCGGCCCC GGGGGACGCA
1201 GTAGCCGAGA TCGACGCTCT CTATGACGTC TACCTGGATG TCCAAGAGAA ATGGGGCTTG
1261 GAGGACGTCA TGTGATGGG CGACTTCAAT GCGGGCTGCA GCTATGTGAG ACCCTCCCAG
1321 TGGTCATCCA TCCGCCTGTG GACAAGCCCC ACCTTCCAGT GGCTGATCCC CGACAGCGCT
1381 GACACCACAG CTACACCCAC GCACTGTGCC TATGACAGGA TCGTGGTTGC AGGGATGCTG
1441 CTCCGAGGGG CCGTTGTTCC CGACTCGGCT CTTCCCTTTA ACTTCCAGGC TGCCTATGGC
1501 CTGAGTGACC AACTGGCCCA AGCCATCAGT GACCACTATC CAGTGGAGGT GATGCTGAAG
1561 TGA

```

//

**Fig. 5(C)**

5' ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC  
 ---  
 M G W S C I I L F L V A T A T G V H

63 72 81 90 99 108  
 TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA  
 ---  
 S Q V Q L V Q S G A E V K K P G A S

117 126 135 144 153 162  
 GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG  
 ---  
 V K V S C K A S G Y T F S A Y W I E

171 180 189 198 207 216  
 TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT  
 ---  
 W V R Q A P G K G L E W V G E I L P

225 234 243 252 261 270  
 GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT  
 ---  
 G S N N S R Y N E K F K G R V T V T

279 288 297 306 315 324  
 AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG  
 ---  
 R D T S T N T A Y M E L S S L R S E

333 342 351 360 369 378  
 GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC  
 ---  
 D T A V Y Y C A R S Y D F A W F A Y

387 396 405 414 423 432  
 TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG  
 ---  
 W G Q G T L V T V S S A S T K G P S

441 450 459 468 477 486  
 GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG  
 ---  
 V F P L A P S S K S T S G G T A A L

495 504 513 522 531 540  
 GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA  
 ---  
 G C L V K D Y F P E P V T V S W N S

549 558 567 576 585 594  
 GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA  
 ---  
 G A L T S G V H T F P A V L Q S S G

**Fig. 5(D)**  
**(Sheet 1 of 3)**





## pAS27

LOCUS PAS27.DNA 1584 bp mRNA PRI 06-MAR-1995  
DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I with SV40  
NLS(construct 1)  
ACCESSION  
NID  
KEYWORDS DNase I.  
SOURCE DNase I sequence is from assembled oligos (thus modified c/f  
MHDNASE1.dna)  
ORGANISM Homo sapiens  
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;  
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.  
TITLE Recombinant human DNase I reduces the viscosity of cystic fibrosis  
sputum  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)  
MEDLINE 91067672  
BASE COUNT 354 a 474 c 446 g 310 t  
ORIGIN

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1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCAAGTGC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACCTCA
541 GCGCGCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAACTC ACACATGCCC ACCGTGCCCCA GCACCTGAAG GGAGCGGCGG GCTGAAGATC
781 GCAGCCTTCA ACATCCAGAC ATTTGGGGGAG ACCAAGATGT CCAATGCCAC CCTCGTCAGC
841 TACATTGTGC AGATCCTGAG CCGCTACGAC ATCGCCCTGG TCCAGGAGGT CAGAGACAGC
901 CACCTGACTG CCGTGGGGAA GCTGCTGGAC AACCTCAATC AGGACGCACC AGACACCTAT
961 CACTACGTGG TCAGTGAGCC ACTGGGACGG AACAGCTATA AGGAGCGCTA CCTGTTCGTG
1021 TACAGGCCTG ACCAGGTGTC TGCGGTGGAC AGCTACTACT ACGATGATGG CTGCGAGCCC
1081 TGCGGGAACG ACACCTTCAA CCGAGAGCCA GCCATTGTCA GGTTCTTCTC CCGTTTACA
1141 GAGGTCAGGG AGTTTGCCAT TGTTCCCCTG CATGCGGCCC CGGGGGACGC AGTAGCCGAG
1201 ATCGACGCTC TCTATGACGT CTACCTGGAT GTCCAAGAGA AATGGGGCTT GGAGGACGTC
1261 ATGTTGATGG GCGACTTCAA TGCGGGCTGC AGCTATGTGA GACCCTCCCA GTGGTCATCC
1321 ATCCGCCTGT GGACAAGCCC CACCTTCCAG TGGCTGATCC CCGACAGCGC TGACACCACA
1381 GCTACACCCA CGCACTGTGC CTATGACAGG ATCGTGGTTG CAGGGATGCT GCTCCGAGGG
1441 GCCGTTGTTC CCGACTCGGC TCTTCCCTTT AACTTCCAGG CTGCCTATGG CCTGAGTGAC
1501 CAACTGGCCC AAGCCATCAG TGACCACTAT CCAGTGGAGG TGATGCTGAA GGGGGGCGGA
1561 CCCAAAAAGA AGCGCAAGGT TTGA
```

//

*Fig. 6(A)*



LOCUS FDDNASE27\_ 1584 BP SS-DNA SYN 25-AUG-2000

DEFINITION -

ACCESSION -

KEYWORDS -

SOURCE -

FEATURES

Location/Qualifiers

frag join(1..>720,<787..1584)

/note="1 to 1584 of 27.dna [Split]"

frag 721..786

/note="1 to 66 of 23/27linker"

frag join(721..>735,<736..786)

/note="1 to 78 of 102linker [Split]"

BASE COUNT 354 A 472 C 447 G 311 T 0 OTHER

ORIGIN -

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG

61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGCCTCAGT GAAGGTGTCC

121 TGCAAGGCTT CTGGCTACAC CTTAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA

181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT

241 GAGAAATTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG

301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC

361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC

421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG

481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGGTGTC GTGGAAGTCA

541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC

601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC

661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT

721 GACAAAACCT ACACATGTCC ACCGTGTCCA GCACCAGAGG GGAGCGGCGG GCTGAAGATC

781 GCAGCCTTCA ACATCCAGAC ATTTGGGGAG ACCAAGATGT CCAATGCCAC CCTCGTCAGC

841 TACATTGTGC AGATCCTGAG CCGCTACGAC ATCGCCCTGG TCCAGGAGGT CAGAGACAGC

901 CACCTGACTG CCGTGGGGAA GCTGCTGGAC AACCTCAATC AGGACGCACC AGACACCTAT

961 CACTACGTGG TCAGTGAGCC ACTGGGACGG AACAGCTATA AGGAGCGCTA CCTGTTCTGT

1021 TACAGGCCTG ACCAGGTGTC TGCGGTGGAC AGCTACTACT ACGATGATGG CTGCGAGCCC

1081 TGCGGGAACG ACACCTTCAA CCGAGAGCCA GCCATTGTCA GGTTCTTCTC CCGGTTTACA

1141 GAGGTCAGGG AGTTTGCCAT TGTTCCCTTG CATGCGGCCC CGGGGGACGC AGTAGCCGAG

1201 ATCGACGCTC TCTATGACGT CTACCTGGAT GTCCAAGAGA AATGGGGCTT GGAGGACGTC

1261 ATGTTGATGG GCGACTTCAA TGCGGGCTGC AGCTATGTGA GACCCTCCCA GTGGTCATCC

1321 ATCCGCCTGT GGACAAGCCC CACCTTCCAG TGGCTGATCC CCGACAGCGC TGACACCACA

1381 GCTACACCCA CGCACTGTGC CTATGACAGG ATCGTGTTG CAGGGATGCT GCTCCGAGGG

1441 GCCGTTGTTT CCGACTCGGC TCTTCCCTTT AACTTCCAGG CTGCCTATGG CCTGAGTGAC

1501 CAACTGGCCC AAGCCATCAG TGACCACTAT CCAGTGAGAG TGATGCTGAA GGGGGGCGGA

1561 CCCAAAAAGA AGCGCAAGGT TTGA

//

**Fig. 6(B)**

LOCUS FDDNASE27K 1593 BP SS-DNA SYN 29-AUG-2000

DEFINITION -

ACCESSION -

KEYWORDS -

SOURCE -

FEATURES Location/Qualifiers

frag 10..1593

/note="1 to 1584 of FdDNase27correct"

frag join(10..>729,<796..1593)

/note="1 to 1584 of 27.dna [Split]"

frag 730..795

/note="1 to 66 of 23/27linker"

frag join(730..>744,<745..795)

/note="1 to 78 of 102linker [Split]"

BASE COUNT 355 A 478 C 449 G 311 T 0 OTHER

ORIGIN -

1 GCCGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTGTC

61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG

121 AAGGTGTCCT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC

181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATTT TACCTGGAAG TAATAATTCT

241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA

301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA

361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA

421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCCT CCTCCAAGAG CACCTCTGGG

481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTCTG

541 TGGAACTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA

601 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC

661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC

721 AAATCTTGTG ACAAACTCA CACATGTCCA CCGTGTCCAG CACCAGAGGG GAGCGGCGGG

781 CTGAAGATCG CAGCCTTCAA CATCCAGACA TTTGGGGAGA CCAAGATGTC CAATGCCACC

841 CTCGTCAGCT ACATTGTGCA GATCCTGAGC CGCTACGACA TCGCCCTGGT CCAGGAGGTC

901 AGAGACAGCC ACCTGACTGC CGTGGGGAAG CTGCTGGACA ACCTCAATCA GGACGCACCA

961 GACACCTATC ACTACGTGGT CAGTGAGCCA CTGGGACGGA ACAGCTATAA GGAGCGCTAC

1021 CTGTTCTGTG ACAGGCCTGA CCAGGTGTCT GCGGTGGACA GCTACTACTA CGATGATGGC

1081 TGCGAGCCCT GCGGGAACGA CACCTTCAAC CGAGAGCCAG CCATTGTCTAG GTTCTTCTCC

1141 CGGTTCACAG AGGTGAGGGA GTTTGCCATT GTTCCCCTGC ATGCGGCCCC GGGGGACGCA

1201 GTAGCCGAGA TCGACGCTCT CTATGACGTC TACCTGGATG TCCAAGAGAA ATGGGGCTTG

1261 GAGGACGTCA TGTTGATGGG CGACTTCAAT GCGGGCTGCA GCTATGTGAG ACCCTCCCAG

1321 TGGTCATCCA TCCGCCTGTG GACAAGCCCC ACCTTCCAGT GGCTGATCCC CGACAGCGCT

1381 GACACCACAG CTACACCCAC GCACTGTGCC TATGACAGGA TCGTGGTTGC AGGGATGCTG

1441 CTCCGAGGGG CCGTTGTTCC CGACTCGGCT CTTCCCTTTA ACTTCCAGGC TGCCTATGGC

1501 CTGAGTGACC AACTGGCCCA AGCCATCAGT GACCACTATC CAGTGGAGGT GATGCTGAAG

1561 GGGGGCGGAC CCAAAAAGAA GCGCAAGGTT TGA

//

**Fig. 6(C)**

5'	ATG	GGA	TGG	AGC	TGT	ATC	ATC	CTC	TTC	TTG	GTA	GCA	ACA	GCT	ACA	GGT	GTC	CAC
	M	G	W	S	C	I	I	L	F	L	V	A	T	A	T	G	V	H
	TCC	CAG	GTG	CAG	CTG	GTG	CAG	TCT	GGG	GCA	GAG	GTG	AAA	AAG	CCT	GGG	GCC	TCA
	S	Q	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	A	S
	GTG	AAG	GTG	TCC	TGC	AAG	GCT	TCT	GGC	TAC	ACC	TTC	AGT	GCC	TAC	TGG	ATA	GAG
	V	K	V	S	C	K	A	S	G	Y	T	F	S	A	Y	W	I	E
	TGG	GTG	CGC	CAG	GCT	CCA	GGA	AAG	GGC	CTC	GAG	TGG	GTC	GGA	GAG	ATT	TTA	CCT
	W	V	R	Q	A	P	G	K	G	L	E	W	V	G	E	I	L	P
	GGA	AGT	AAT	AAT	TCT	AGA	TAC	AAT	GAG	AAG	TTC	AAG	GGC	CGA	GTG	ACA	GTC	ACT
	G	S	N	N	S	R	Y	N	E	K	F	K	G	R	V	T	V	T
	AGA	GAC	ACA	TCC	ACA	AAC	ACA	GCC	TAC	ATG	GAG	CTC	AGC	AGC	CTG	AGG	TCT	GAG
	R	D	T	S	T	N	T	A	Y	M	E	L	S	S	L	R	S	E
	GAC	ACA	GCC	GTC	TAT	TAC	TGT	GCA	AGA	TCC	TAC	GAC	TTT	GCC	TGG	TTT	GCT	TAC
	D	T	A	V	Y	Y	C	A	R	S	Y	D	F	A	W	F	A	Y
	TGG	GGC	CAA	GGG	ACT	CTG	GTC	ACA	GTC	TCC	TCA	GCC	TCC	ACC	AAG	GGC	CCA	TCG
	W	G	Q	G	T	L	V	T	V	S	S	A	S	T	K	G	P	S
	GTC	TTC	CCC	CTG	GCA	CCC	TCC	TCC	AAG	AGC	ACC	TCT	GGG	GGC	ACA	GCG	GCC	CTG
	V	F	P	L	A	P	S	S	K	S	T	S	G	G	T	A	A	L
	GGC	TGC	CTG	GTC	AAG	GAC	TAC	TTC	CCC	GAA	CCG	GTG	ACG	GTG	TCG	TGG	AAC	TCA
	G	C	L	V	K	D	Y	F	P	E	P	V	T	V	S	W	N	S
	GGC	GCC	CTG	ACC	AGC	GGC	GTG	CAC	ACC	TTC	CCG	GCT	GTC	CTA	CAG	TCC	TCA	GGA
	G	A	L	T	S	G	V	H	T	F	P	A	V	L	Q	S	S	G

**Fig. 6(D)**  
(Sheet 1 of 3)

603	612	621	630	639	648
CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG					
L Y S L S S V V T V P S S S L G T Q					
657	666	675	684	693	702
ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA					
T Y I C N V N H K P S N T K V D K K					
711	720	729	738	747	756
GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT					
V E P K S C D K T H T C P P C P A P					
765	774	783	792	801	810
GAA GGG AGC GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG					
E G S G G L K I A A F N I Q T F G E					
819	828	837	846	855	864
ACC AAG ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC					
T K M S N A T L V S Y I V Q I L S R					
873	882	891	900	909	918
TAC GAC ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG					
Y D I A L V Q E V R D S H L T A V G					
927	936	945	954	963	972
AAG CTG CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC					
K L L D N L N Q D A P D T Y H Y V V					
981	990	999	1008	1017	1026
AGT GAG CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG					
S E P L G R N S Y K E R Y L F V Y R					
1035	1044	1053	1062	1071	1080
CCT GAC CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC					
P D Q V S A V D S Y Y Y D D G C E P					
1089	1098	1107	1116	1125	1134
TGC GGG AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC TCC CGG					
C G N D T F N R E P A I V R F F S R					
1143	1152	1161	1170	1179	1188
TTC ACA GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC					
F T E V R E F A I V P L H A A P G D					
1197	1206	1215	1224	1233	1242

**Fig. 6(D)**  
(Sheet 2 of 3)

[illegible]

**Fig. 6D**  
(Sheet 3 of 3)

## pAS34

LOCUS PAS34.DNA 2196 bp 2196 bp 2196 bp DNA 14-AUG-1998  
 DEFINITION HUMANISED HMFG1 heavy chain fused to human DNase construct 34  
 DEFINITION Clone 16.4.2 (same as hcdnasel.dna template file)  
 REFERENCE  
 AUTHORS VERHOEYEN ET AL  
 TITLE CONSTRUCTION OF RESHAPED HMFG1 etc  
 JOURNAL IMMUNOL. (1993):78, 364-370  
 COMMENT Human DNase sequence is modified as a result of oligo assembly (mhdnase.dna)  
 COMMENT The fusion was made using overlapping oligos AS79 and AS80  
 FEATURES AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A)  
 FEATURES Residue 963 is G > T leading to silent mutation in all clones  
 SITES Note  
 BASE COUNT 501 a 677 c 607 g 411 t  
 ORIGIN ?

```

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAAGTCA
541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAACTC ACACATGCCC ACCGTGCCCC GCACCTGAAC TCCTGGGGGG ACCGTCAGTC
781 TTCCTCTTCC CCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA
841 TCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC
901 GCGTGGGAG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA GACACGTAC
961 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG
1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA
1081 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG
1141 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG
1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC
1261 GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG
1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC
1381 CTCTCCCTGT CTCCGGGTAA AGGGAGCGGC GGGCTGAAGA TCGCAGCCTT CAACATCCAG
1441 ACATTTGGGG AGACCAAGAT GTCCAATGCC ACCCTCGTCA GCTACATTGT GCAGATCCTG
1501 AGCCGCTACG ACATCGCCCT GGTCCAGGAG GTCAGAGACA GCCACCTGAC TGCCGTGGGG
1561 AAGCTGCTGG ACAACCTCAA TCAGGACGCA CCAGACACCT ATCACTACGT GGTCACTGAG
1621 CCACTGGGAC GGAACAGCTA TAAGGAGCGC TACCTGTTTC TGTACAGGCC TGACCAGGTG
1681 TCTGCGGTGG ACAGCTACTA CTACGATGAT GGCTGCGAGC CCTGCGGGAA CGACACCTTC
1741 AACCAGAGAG CAGCCATTGT CAGGTTCTTC TCCCGGTTCA CAGAGGTCAG GGAGTTTGCC
1801 ATTGTTCCCC TGCATGCGGC CCCGGGGGAC GCAGTAGCCG AGATCGACGC TCTCTATGAC
1861 GTCTACCTGG ATGTCCAAGA GAAATGGGGC TTGGAGGACG TCATGTTGAT GGGCGACTTC
1921 AATGCGGGCT GCAGCTATGT GAGACCTTCC CAGTGGTCAT CCATCCGCTT GTGGACAAGC
1981 CCCACCTTCC AGTGGCTGAT CCCCAGACAG GCTGACACCA CAGCTACACC CACGCACTGT
2041 GCCTATGACA GGATCGTGGT TGCAGGGATG CTGCTCCGAG GGGCCGTTGT TCCCGACTCG
2101 GCTCTTCCCT TTAACCTCCA GGCTGCCTAT GGCCTGAGTG ACCAACTGGC CCAAGCCATC
2161 AGTGACCACT ATCCAGTGGA GGTGATGCTG AAGTGA
  
```

//

**Fig. 7(A)**

[illegible]

- 1 -





1359	1368	1377	1386	1395	1404
GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG GGT AAA GGG					
---	---	---	---	---	---
A L H N H Y T Q K S L S L S P G K <u>G</u>					
1413	1422	1431	1440	1449	1458
AGC GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG					
---	---	---	---	---	---
<u>S G G</u> L K I A A F N I Q T F G E T K					
1467	1476	1485	1494	1503	1512
ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC					
---	---	---	---	---	---
M S N A T L V S Y I V Q I L S R Y D					
1521	1530	1539	1548	1557	1566
ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG					
---	---	---	---	---	---
I A L V Q E V R D S H L T A V G K L					
1575	1584	1593	1602	1611	1620
CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG					
---	---	---	---	---	---
L D N L N Q D A P D T Y H Y V V S E					
1629	1638	1647	1656	1665	1674
CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC					
---	---	---	---	---	---
P L G R N S Y K E R Y L F V Y R P D					
1683	1692	1701	1710	1719	1728
CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG					
---	---	---	---	---	---
Q V S A V D S Y Y Y D D G C E P C G					
1737	1746	1755	1764	1773	1782
AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC TCC CGG TTC ACA					
---	---	---	---	---	---
N D T F N R E P A I V R F F S R F T					
1791	1800	1809	1818	1827	1836
GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA					
---	---	---	---	---	---
E V R E F A I V P L H A A P G D A V					
1845	1854	1863	1872	1881	1890
GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC					
---	---	---	---	---	---
A E I D A L Y D V Y L D V Q E K W G					
1899	1908	1917	1926	1935	1944
TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA					
---	---	---	---	---	---
L E D V M L M G D F N A G C S Y V R					
1953	1962	1971	1980	1989	1998
CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG					
---	---	---	---	---	---
P S Q W S S I R L W T S P T F Q W L					
2007	2016	2025	2034	2043	2052
ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG					
---	---	---	---	---	---
I P D S A D T T A T P T H C A Y D R					

**Fig. 7(B)**  
(Sheet 3 of 4)



## pAS35

LOCUS PAS35.DNA 2193 bp 2193 bp DNA 14-AUG-1998  
 DEFINITION HUMANISED HMFG1 heavy chain fused to human DNase construct 35  
 DEFINITION Clone 17.12.1 with silent K to K mutation (1398 A > G)  
 REFERENCE  
 AUTHORS VERHOEYEN ET AL  
 TITLE CONSTRUCTION OF RESHAPED HMFG1 etc  
 JOURNAL IMMUNOL. (1993):78, 364-370  
 COMMENT Human DNase sequence is modified as a result of oligo assembly (mhdnase.dna)  
 COMMENT The fusion was made using overlapping oligos AS81 and AS82  
 FEATURES AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A)  
 FEATURES Residue 963 is G > T leading to silent mutation in all clones  
 FEATURES In 17.12.1 residue 1398 is A > G (silent K to K mutation)  
 SITES Note  
 BASE COUNT 500 a 677 c 606 g 410 t  
 ORIGIN ?

```

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCACTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATAACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTG GTGGAACCTCA
541 GCGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAATC ACACATGCCC ACCGTGCCCA GCACCTGAAC TCCTGGGGGG ACCGTGAGTC
781 TTCCTCTTCC CCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA
841 TGCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC
901 GGCGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC
961 CGTGTGGTCA GCGTCCTCAC CGTCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG
1021 TGCAAGGTCT CCAACAAAGC CCTCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA
1081 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCGGGGATGA GCTGACCAAG
1141 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG
1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC
1261 GACGGCTCCT TCTTCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG
1321 AACGTCTTCT CATGCTCCGT GATGCTAGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC
1381 CTCTCCCTGT CTCCGAAGGG GAGCGGCGGG CTGAAGATCG CAGCCTTCAA CATCCAGACA
1441 TTTGGGGAGA CCAAGATGTC CAATGCCACC CTCGTCAGCT ACATTGTGCA GATCCTGAGC
1501 CGCTACGACA TCGCCCTGGT CCAGGAGGTC AGAGACAGCC ACCTGACTGC CGTGGGGAAG
1561 CTGCTGGACA ACCTCAATCA GGACGCACCA GACACCTATC ACTACGTGGT CAGTGAGCCA
1621 CTGGGACGGA ACAGCTATAA GGAGCGCTAC CTGTTCTGTG ACAGGCCTGA CCAGGTGTCT
1681 GCGGTGGACA GCTACTACTA CGATGATGGC TGCGAGCCCT GCGGGAACGA CACCTTCAAC
1741 CGAGAGCCAG CCATTGTCAG GTTCTTCTCC CGGTTACAG AGGTCAGGGA GTTTGCCATT
1801 GTTCCCCTGC ATGCGGCCCC GGGGACGCA GTAGCCGAGA TCGACGCTCT CTATGACGTC
1861 TACCTGGATG TCCAAGAGAA ATGGGGCTTG GAGGACGTCA TGTTGATGGG CGACTTCAAT
1921 GCGGGCTGCA GCTATGTGAG ACCCTCCCAG TGGTCATCCA TCCGCCTGTG GACAAGCCCC
1981 ACCTTCCAGT GGCTGATCCC CGACAGCGCT GACACCACAG CTACACCCAC GCACTGTGCC
2041 TATGACAGGA TCGTGGTTGC AGGGATGCTG CTCCGAGGGG CCGTTGTTCC CGACTCGGCT
2101 CTTCCCTTTA ACTTCCAGGC TGCCTATGGC CTGAGTGACC AACTGGCCCA AGCCATCAGT
2161 GACCACTATC CAGTGGAGGT GATGCTGAAG TGA

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*Fig. 8(A)*









# pAS36

LOCUS PAS36.DNA 2190 bp 2190 bp DNA 14-AUG-1998

DEFINITION HUMANISED HMFG1 heavy chain fused to human DNase - construct 36

DEFINITION Clone 18.24.1 with residue 1392 T > C

REFERENCE

AUTHORS VERHOEYEN ET AL

TITLE CONSTRUCTION OF RESHAPED HMFG1 etc

JOURNAL IMMUNOL. (1993):78, 364-370

COMMENT Human DNase sequence is modified as a result of oligo assembly (mhdnase.dna)

COMMENT The fusion was made using overlapping oligos AS83 and AS84

FEATURES AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A)

FEATURES Residue 963 is G > T leading to silent mutation in all clones

FEATURES Residue 1392 T > C silent S to S mutation

SITES Note

BASE COUNT 498 a 678 c 605 g 409 t

ORIGIN ?

```

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCAAGTGC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAAGTCA
541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAACTC ACACATGCCC ACCGTGCCCC GCACCTGAAC TCCTGGGGGG ACCGTCAGTC
781 TTCCTCTTCC CCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA
841 TGCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC
901 GCGGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC
961 CGTGTGGTCA GCGTCCTCAC CGTCTGTCAC CAGGACTGGC TGAATGGCAA GGAGTCAAG
1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA
1081 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG
1141 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG
1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC
1261 GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG
1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC
1381 CTCTCCCTGT CcCCGGGGAG CGGCGGGCTG AAGATCGCAG CCTTCAACAT CCAGACATTT
1441 GGGGAGACCA AGATGTCCAA TGCCACCCTC GTCAGCTACA TTGTGCAGAT CCTGAGCCGC
1501 TACGACATCG CCCTGGTCCA GGAGGTCAGA GACAGCCACC TGAAGTCCGT GGGGAAGCTG
1561 CTGGACAACC TCAATCAGGA CGCACCAGAC ACCTATCACT ACGTGGTCAG TGAGCCACTG
1621 GGACGGAACA GCTATAAGGA GCGCTACCTG TTCGTGTACA GGCCTGACCA GGTGTCTGCG
1681 GTGGACAGCT ACTACTACGA TGATGGCTGC GAGCCCTGCG GGAACGACAC CTTCAACCGA
1741 GAGCCAGCCA TTGTGAGGTT CTTCTCCCGG TTCACAGAGG TCAGGGAGTT TGCCATTGTT
1801 CCCCTGCATG CGGCCCCGGG GGACGCAGTA GCCGAGATCG ACGCTCTCTA TGACGTCTAC
1861 CTGGATGTCC AAGAGAAATG GGGCTTGAG GACGTCATGT TGATGGGCGA CTTCAATGCG
1921 GGCTGCAGCT ATGTGAGACC CTCCCAGTGG TCATCCATCC GCCTGTGGAC AAGCCCCACC
1981 TTCCAGTGGC TGATCCCCGA CAGCGCTGAC ACCACAGCTA CACCCACGCA CTGTGCCTAT
2041 GACAGGATCG TGGTTGCAGG GATGCTGCTC CGAGGGGCGG TTGTTCCCGA CTCGGCTCTT
2101 CCCTTTAACT TCCAGGCTGC CTATGGCCTG AGTGACCAAC TGGCCCAAGC CATCAGTGAC
2161 CACTATCCAG TGGAGGTGAT GCTGAAGTGA

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**Fig. 9(A)**







1359	1368	1377	1386	1395	1404
GCT CTG CAC AAC CAC TAC	ACG CAG AAG AGC CTC	TCC CTG TCC CCG GGG	AGC GGC		
-----					
A L H N H Y T Q K S L S L S P	<u>G S G</u>				
-----					
1413	1422	1431	1440	1449	1458
GGG CTG AAG ATC GCA GCC TTC	AAC ATC CAG ACA TTT	GGG GAG ACC AAG	ATG TCC		
-----					
<u>G</u> L K I A A F N I Q T F G E T K M S					
-----					
1467	1476	1485	1494	1503	1512
AAT GCC ACC CTC GTC AGC TAC	ATT GTG CAG ATC CTG	AGC CGC TAC GAC	ATC GCC		
-----					
N A T L V S Y I V Q I L S R Y D I A					
-----					
1521	1530	1539	1548	1557	1566
CTG GTC CAG GAG GTC AGA GAC	AGC CAC CTG ACT GCC	GTG GGG AAG CTG	CTG GAC		
-----					
L V Q E V R D S H L T A V G K L L D					
-----					
1575	1584	1593	1602	1611	1620
AAC CTC AAT CAG GAC GCA CCA	GAC ACC TAT CAC TAC	GTG GTC AGT GAG	CCA CTG		
-----					
N L N Q D A P D T Y H Y V V S E P L					
-----					
1629	1638	1647	1656	1665	1674
GGA CGG AAC AGC TAT AAG GAG	CGC TAC CTG TTC GTG	TAC AGG CCT GAC	CAG GTG		
-----					
G R N S Y K E R Y L F V Y R P D Q V					
-----					
1683	1692	1701	1710	1719	1728
TCT GCG GTG GAC AGC TAC TAC	TAC GAT GAT GGC TGC	GAG CCC TGC GGG	AAC GAC		
-----					
S A V D S Y Y Y D D G C E P C G N D					
-----					
1737	1746	1755	1764	1773	1782
ACC TTC AAC CGA GAG CCA GCC	ATT GTC AGG TTC TTC	TCC CGG TTC ACA	GAG GTC		
-----					
T F N R E P A I V R F F S R F T E V					
-----					
1791	1800	1809	1818	1827	1836
AGG GAG TTT GCC ATT GTT CCC	CTG CAT GCG GCC CCG	GGG GAC GCA GTA	GCC GAG		
-----					
R E F A I V P L H A A P G D A V A E					
-----					
1845	1854	1863	1872	1881	1890
ATC GAC GCT CTC TAT GAC GTC	TAC CTG GAT GTC CAA	GAG AAA TGG GGC	TTG GAG		
-----					
I D A L Y D V Y L D V Q E K W G L E					
-----					
1899	1908	1917	1926	1935	1944
GAC GTC ATG TTG ATG GGC GAC	TTC AAT GCG GGC TGC	AGC TAT GTG AGA	CCC TCC		
-----					
D V M L M G D F N A G C S Y V R P S					
-----					
1953	1962	1971	1980	1989	1998
CAG TGG TCA TCC ATC CGC CTG	TGG ACA AGC CCC ACC	TTC CAG TGG CTG	ATC CCC		
-----					
Q W S S I R L W T S P T F Q W L I P					
-----					
2007	2016	2025	2034	2043	2052
GAC AGC GCT GAC ACC ACA GCT	ACA CCC ACG CAC TGT	GCC TAT GAC AGG	ATC GTG		
-----					
D S A D T T A T P T H C A Y D R I V					

**Fig. 9(B)**  
(Sheet 3 of 4)

2061	2070	2079	2088	2097	2106
GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG GCT CTT CCC TTT					
---	---	---	---	---	---
V A G M L L R G A V V P D S A L P F					
2115	2124	2133	2142	2151	2160
AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA GCC ATC AGT GAC					
---	---	---	---	---	---
N F Q A A Y G L S D Q L A Q A I S D					
2169	2178	2187			
CAC TAT CCA GTG GAG GTG ATG CTG AAG TGA 3'					
---	---	---	---	---	---
H Y P V E V M L K *					

***Fig. 9(B)***  
***(Sheet 4 of 4)***

## pAS37

LOCUS PAS37.DNA 2226 bp 2196 bp 2196 bp DNA 14-AUG-1998  
DEFINITION HUMANISED HMFG1 heavy chain fused to human DNase construct 37  
DEFINITION Clone 16.4.2 (same as hcdnasel.dna template file) plus NLS  
REFERENCE  
AUTHORS VERHOEYEN ET AL  
TITLE CONSTRUCTION OF RESHAPED HMFG1 etc  
JOURNAL IMMUNOL. (1993):78, 364-370  
COMMENT Human DNase sequence is modified as a result of oligo assembly (mhdnase.dna)  
COMMENT The fusion was made using overlapping oligos AS79 and AS80  
FEATURES AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A)  
FEATURES Residue 963 is G > T leading to silent mutation in all clones  
SITES Note  
BASE COUNT 511 a 683 c 619 g 413 t  
ORIGIN ?

```
1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCAAGTGC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACCTA
541 GCGGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAATC ACACATGCCC ACCGTGCCCA GCACCTGAAC TCCTGGGGGG ACCGTGAGTC
781 TTCCTCTTCC CCCCCAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA
841 TGCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC
901 GCGGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC
961 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG
1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA
1081 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG
1141 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG
1201 TGGGAGAGCA ATGGGAGGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC
1261 GACGGCTCCT TCTTCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG
1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC
1381 CTCTCCCTGT CTCCGGGTAA AGGGAGCGGC GGGCTGAAGA TCGCAGCCTT CAACATCCAG
1441 ACATTTGGGG AGACCAAGAT GTCCAATGCC ACCCTCGTCA GCTACATTGT GCAGATCCTG
1501 AGCCGCTACG ACATCGCCCT GGTCCAGGAG GTCAGAGACA GCCACCTGAC TGCCGTGGGG
1561 AAGCTGCTGG ACAACCTCAA TCAGGACGCA CCAGACACCT ATCACTACGT GGTCACTGAG
1621 CCACTGGGAG GGAACAGCTA TAAGGAGCGC TACCTGTTTCG TGTACAGGCC TGACCAGGTG
1681 TCTGCGGTGG ACAGCTACTA CTACGATGAT GGCTGCGAGC CCTGCGGGAA CGACACCTTC
1741 AACCAGAGAG CAGCCATTGT CAGGTTCTTC TCCCGGTTCA CAGAGGTCAG GGAGTTTGCC
1801 ATTGTTCCCC TGCATGCGGC CCCGGGGGAC GCAGTAGCCG AGATCGACGC TCTCTATGAC
1861 GTCTACCTGG ATGTCCAAGA GAAATGGGGC TTGGAGGACG TCATGTTGAT GGGCGACTTC
1921 AATGCGGGCT GCAGCTATGT GAGACCCTCC CAGTGGTCAT CCATCCGCCT GTGGACAAGC
1981 CCCACCTTCC AGTGGCTGAT CCCCAGACGC GCTGACACCA CAGCTACACC CACGCACTGT
2041 GCCTATGACA GGATCGTGGT TGCAGGGATG CTGCTCCGAG GGGCCGTTGT TCCCGACTCG
2101 GCTCTTCCCT TTAACCTCCA GGCTGCCTAT GGCCTGAGTG ACCAACTGGC CCAAGCCATC
2161 AGTGACCACT ATCCAGTGGA GGTGATGCTG AAGGGGGGCG GACCCAAAAA GAAGCGCAAG
2221 GTTTGA
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→ NLS

**Fig. 10(A)**

	<div>9</div>							<div>18</div>			<div>27</div>			<div>36</div>			<div>45</div>			<div>54</div>	
S'	ATG	GGA	TGG	AGC	TGT	ATC	ATC	CTC	TTC	TTG	GTA	GCA	ACA	GCT	ACA	GGT	GTC	CAC			
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
	M	G	W	S	C	I	I	L	F	L	V	A	T	A	T	G	V	H			
	<div>63</div>							<div>72</div>			<div>81</div>			<div>90</div>			<div>99</div>			<div>108</div>	
	TCC	CAG	GTG	CAG	CTG	GTG	CAG	TCT	GGG	GCA	GAG	GTG	AAA	AAG	CCT	GGG	GCC	TCA			
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
	<u>S</u>	Q	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	A	S			
	<div>117</div>							<div>126</div>			<div>135</div>			<div>144</div>			<div>153</div>			<div>162</div>	
	GTG	AAG	GTG	TCC	TGC	AAG	GCT	TCT	GGC	TAC	ACC	TTC	AGT	GCC	TAC	TGG	ATA	GAG			
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
	V	K	V	S	C	K	A	S	G	Y	T	F	S	A	Y	W	I	E			
	<div>171</div>							<div>180</div>			<div>189</div>			<div>198</div>			<div>207</div>			<div>216</div>	
	TGG	GTG	CGC	CAG	GCT	CCA	GGA	AAG	GGC	CTC	GAG	TGG	GTC	GGA	GAG	ATT	TTA	CCT			
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
	W	V	R	Q	A	P	G	K	G	L	E	W	V	G	E	I	L	P			
	<div>225</div>							<div>234</div>			<div>243</div>			<div>252</div>			<div>261</div>			<div>270</div>	
	GGA	ACT	AAT	AAT	TCT	AGA	TAC	AAT	GAG	AAG	TTC	AAG	GGC	CGA	GTG	ACA	GTC	ACT			
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
	G	S	N	N	S	R	Y	N	E	K	F	K	G	R	V	T	V	T			
	<div>279</div>							<div>288</div>			<div>297</div>			<div>306</div>			<div>315</div>			<div>324</div>	
	AGA	GAC	ACA	TCC	ACA	AAC	ACA	GCC	TAC	ATG	GAG	CTC	AGC	AGC	CTG	AGG	TCT	GAG			
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
	R	D	T	S	T	N	T	A	Y	M	E	L	S	S	L	R	S	E			
	<div>333</div>							<div>342</div>			<div>351</div>			<div>360</div>			<div>369</div>			<div>378</div>	
	GAC	ACA	GCC	GTC	TAT	TAC	TGT	GCA	AGA	TCC	TAC	GAC	TTT	GCC	TGG	TTT	GCT	TAC			
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
	D	T	A	V	Y	Y	C	A	R	S	Y	D	F	A	W	F	A	Y			
	<div>387</div>							<div>396</div>			<div>405</div>			<div>414</div>			<div>423</div>			<div>432</div>	
	TGG	GGC	CAA	GGG	ACT	CTG	GTC	ACA	GTC	TCC	TCA	GCC	TCC	ACC	AAG	GGC	CCA	TCG			
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
	W	G	Q	G	T	L	V	T	V	S	S	A	S	T	K	G	P	S			
	<div>441</div>							<div>450</div>			<div>459</div>			<div>468</div>			<div>477</div>			<div>486</div>	
	GTC	TTC	CCC	CTG	GCA	CCC	TCC	TCC	AAG	AGC	ACC	TCT	GGG	GGC	ACA	GCG	GCC	CTG			
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
	V	F	P	L	A	P	S	S	K	S	T	S	G	G	T	A	A	L			
	<div>495</div>							<div>504</div>			<div>513</div>			<div>522</div>			<div>53</div>				

**Fig. 10(B)**  
(Sheet 1 of 4)









## pAS38

LOCUS PAS38.DNA 2223 bp 2193 bp DNA 14-AUG-1998  
 DEFINITION HUMANISED HMFG1 heavy chain fused to human DNase construct 38  
 DEFINITION Clone 17.12.1 with silent K to K mutation (1398 A > G)+NLS  
 REFERENCE  
 AUTHORS VERHOEYEN ET AL  
 TITLE CONSTRUCTION OF RESHAPED HMFG1 etc  
 JOURNAL IMMUNOL. (1993):78, 364-370  
 COMMENT Human DNase sequence is modified as a result of oligo assembly (mhdnase.dna)  
 COMMENT The fusion was made using overlapping oligos AS81 and AS82  
 FEATURES AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A)  
 FEATURES Residue 963 is G > T leading to silent mutation in all clones  
 FEATURES In 17.12.1 residue 1398 is A > G (silent K to K mutation)  
 SITES Note  
 BASE COUNT 510 a 683 c 618 g 412 t  
 ORIGIN ?

```

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACCTA
541 GCGGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAG CTACATCTGC
661 AACGTGAATC ACAAGCCCAG ACACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAACTC ACACATGCCC ACCGTGCCCC GCACCTGAAC TCCTGGGGGG AGCCTCAGTC
781 TTCCTCTTCC CCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA
841 TCGGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC
901 GGCGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC
961 CGTGTGGTCA GCGTCCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG
1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA
1081 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG
1141 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG
1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC
1261 GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG
1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC
1381 CTCTCCCTGT CTCCGAAGGG GAGCGGCGGG CTGAAGATCG CAGCCTTCAA CATCCAGACA
1441 TTTGGGGAGA CCAAGATGTC CAATGCCACC CTCGTCAGCT ACATTGTGCA GATCCTGAGC
1501 CGCTACGACA TCGCCCTGGT CCAGGAGGTC AGAGACAGCC ACCTGACTGC CGTGGGGAAG
1561 CTGCTGGACA ACCTCAATCA GGACGCACCA GACACCTATC ACTACGTGGT CAGTGAGCCA
1621 CTGGGACGGA ACAGCTATAA GGAGCGCTAC CTGTTCGTGT ACAGGCCTGA CCAGGTGTCT
1681 GCGGTGGACA GCTACTACTA CGATGATGGC TGCGAGCCCT GCGGGAACGA CACCTTCAAC
1741 CGAGAGCCAG CCATTGTCAG GTTCTTCTCC CGGTTACAG AGGTCAGGGA GTTTGCCATT
1801 GTTCCCCTGC ATGCGGCCCC GGGGGACGCA GTAGCCGAGA TCGACGCTCT CTATGACGTC
1861 TACCTGGATG TCCAAGAGAA ATGGGGCTTG GAGGACGTCA TGTTGATGGG CGACTTCAAT
1921 GCGGGCTGCA GCTATGTGAG ACCCTCCCAG TGGTCATCCA TCCGCCTGTG GACAAGCCCC
1981 ACCTTCCAGT GGCTGATCCC CGACAGCGCT GACACCACAG CTACACCCAC GCACTGTGCC
2041 TATGACAGGA TCGTGATTGC AGGGATGCTG CTCCGAGGGG CCGTTGTTCC CGACTCGGCT
2101 CTTCCCTTTA ACTTCCAGGC TGCCTATGGC CTGAGTGACC AACTGGCCCA AGCCATCAGT
2161 GACCACTATC CAGTGGAGGT GATGCTGAAG GGGGGCGGAC CCAAAAAGAA GCGCAAGGTT
2221 TGA

```

//

└─NLS

*Fig. 11(A)*







2061	2070	2079	2088	2097	2106
GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG GCT CTT CCC					
---	---	---	---	---	---
V V A G M L L R G A V V P D S A L P					

2115	2124	2133	2142	2151	2160
TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA GCC ATC AGT					
---	---	---	---	---	---
F N F Q A A Y G L S D Q L A Q A I S					

2169	2178	2187	2196	2205	2214
GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG GGG GGC GGA CCC AAA AAG AAG CGC					
---	---	---	---	---	---
D H Y P V E V M L K	<u>G</u>	<u>G</u>	<u>G</u>	<u>P</u>	<u>K</u> <u>K</u> <u>K</u> <u>R</u>

2223
AAG GTT TGA 3'
---
K V *
=====

***Fig. 11(D)***  
***(Sheet 4 of 4)***

## pAS39

LOCUS PAS39.DNA 2220 bp 2190 bp DNA 14-AUG-1998  
DEFINITION HUMANISED HMFG1 heavy chain fused to human DNase - construct 39  
DEFINITION Clone 18.24.1 with residue 1392 T > C +NLS  
REFERENCE  
AUTHORS VERHOEYEN ET AL  
TITLE CONSTRUCTION OF RESHAPED HMFG1 etc  
JOURNAL IMMUNOL. (1993):78, 364-370  
COMMENT Human DNase sequence is modified as a result of oligo assembly (mhdnase.dna)  
COMMENT The fusion was made using overlapping oligos AS83 and AS84  
FEATURES AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A)  
FEATURES Residue 963 is G > T leading to silent mutation in all clones  
FEATURES Residue 1392 T > C silent S to S mutation  
SITES Note  
BASE COUNT 508 a 684 c 617 g 411 t  
ORIGIN ?

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG  
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC  
121 TGCAAGGCTT CTGGCTACAC CTTAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA  
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT  
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG  
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC  
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC  
421 AAGGGCCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG  
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACCTCA  
541 GCGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC  
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC  
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT  
721 GACAAAACCTC ACACATGCCC ACCGTGCCCC GCACCTGAAC TCCTGGGGGG ACCGTCAAGT  
781 TTCCTCTTCC CCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA  
841 TGGCTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC  
901 GCGGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA GAGCAGTAC  
961 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAA  
1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA  
1081 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG  
1141 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG  
1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC  
1261 GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG  
1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC  
1381 CTCTCCCTGT CcCCGGGGAG CGGCGGGCTG AAGATCGCAG CCTTCAACAT CCAGACATTT  
1441 GGGGAGACCA AGATGTCCAA TGCCACCCTC GTCAGCTACA TTGTGCAGAT CCTGAGCCGC  
1501 TACGACATCG CCCTGGTCCA GGAGGTCAGA GACAGCCACC TGAATGCCGT GGGGAAGCTG  
1561 CTGGACAACC TCAATCAGGA CGCACCAGAC ACCTATCACT ACGTGGTCAG TGAGCCACTG  
1621 GGACGGAACA GCTATAAGGA GCGCTACCTG TTCGTGTACA GGCCTGACCA GGTGTCTGCG  
1681 GTGGACAGCT ACTACTACGA TGATGGCTGC GAGCCCTGCG GGAACGACAC CTTCAACCGA  
1741 GAGCCAGCCA TTGTCAGGTT CTTCTCCCGG TTCACAGAGG TCAGGGAGTT TGCCATTGTT  
1801 CCCCTGCATG CGGCCCCGGG GGACGCAGTA GCCGAGATCG ACGCTCTCTA TGACGTCTAC  
1861 CTGGATGTCC AAGAGAAATG GGGCTTGGAG GACGTCATGT TGATGGGCGA CTTCAATGCG  
1921 GGCTGCAGCT ATGTGAGACC CTCCCAGTGG TCATCCATCC GCCTGTGGAC AAGCCCCACC  
1981 TTCCAGTGGC TGATCCCCGA CAGCGCTGAC ACCACAGCTA CACCCACGCA CTGTGCCTAT  
2041 GACAGGATCG TGGTTGCAGG GATGCTGCTC CGAGGGGCCG TTGTTCCCGA CTCGGCTCTT  
2101 CCCTTTAACT TCCAGGCTGC CTATGGCCTG AGTGACCAAC TGGCCCAAGC CATCAGTGAC  
2161 CACTATCCAG TGGAGGTGAT GCTGAAGGGGG GGCGGACCCA AAAAGAAGCG CAAGGTTTGA

//

**Fig. 12(A)**

[illegible]

*[The following section contains extremely faint, illegible text, likely bleed-through from the reverse side of the page.]*



ACC	TAC	ATC	TGC	AAC	GTG	AAT	CAC	AAG	CCC	AGC	AAC	ACC	AAG	GTG	GAC	AAG	AAA				
T	Y	I	C	N	V	N	H	K	P	S	N	T	K	V	D	K	K				
-----																					
711				720				729				738				747				756	
GTT	GAG	CCC	AAA	TCT	TGT	GAC	AAA	ACT	CAC	ACA	TGC	CCA	CCG	TGC	CCA	GCA	CCT				
V	E	P	K	S	C	D	K	T	H	T	C	P	P	C	P	A	P				
-----																					
765				774				783				792				801				810	
GAA	CTC	CTG	GGG	GGA	CCG	TCA	GTC	TTC	CTC	TTC	CCC	CCA	AAA	CCC	AAG	GAC	ACC				
E	L	L	G	G	P	S	V	F	L	F	P	P	K	P	K	D	T				
-----																					
819				828				837				846				855				864	
CTC	ATG	ATC	TCC	CGG	ACC	CCT	GAG	GTC	ACA	TGC	GTG	GTG	GTG	GAC	GTG	AGC	CAC				
L	M	I	S	R	T	P	E	V	T	C	V	V	V	D	V	S	H				
-----																					
873				882				891				900				909				918	
GAA	GAC	CCT	GAG	GTC	AAG	TTC	AAC	TGG	TAC	GTG	GAC	GGC	GTG	GAG	GTG	CAT	AAT				
E	D	P	E	V	K	F	N	W	Y	V	D	G	V	E	V	H	N				
-----																					
927				936				945				954				963				972	
GCC	AAG	ACA	AAG	CCG	CGG	GAG	GAG	CAG	TAC	AAC	AGC	ACG	TAC	CGT	GTG	GTC	AGC				
A	K	T	K	P	R	E	E	Q	Y	N	S	T	Y	R	V	V	S				
-----																					
981				990				999				1008				1017				1026	
GTC	CTC	ACC	GTC	CTG	CAC	CAG	GAC	TGG	CTG	AAT	GGC	AAG	GAG	TAC	AAG	TGC	AAG				
V	L	T	V	L	H	Q	D	W	L	N	G	K	E	Y	K	C	K				
-----																					
1035				1044				1053				1062				1071				1080	
GTC	TCC	AAC	AAA	GCC	CTC	CCA	GCC	CCC	ATC	GAG	AAA	ACC	ATC	TCC	AAA	GCC	AAA				
V	S	N	K	A	L	P	A	P	I	E	K	T	I	S	K	A	K				
-----																					
1089				1098				1107				1116				1125				1134	
GGG	CAG	CCC	CGA	GAA	CCA	CAG	GTG	TAC	ACC	CTG	CCC	CCA	TCC	CGG	GAT	GAG	CTG				
G	Q	P	R	E	P	Q	V	Y	T	L	P	P	S	R	D	E	L				
-----																					
1143				1152				1161				1170				1179				1188	
ACC	AAG	AAC	CAG	GTC	AGC	CTG	ACC	TGC	CTG	GTC	AAA	GGC	TTC	TAT	CCC	AGC	GAC				
T	K	N	Q	V	S	L	T	C	L	V	K	G	F	Y	P	S	D				
-----																					
1197				1206				1215				1224				1233				1242	
ATC	GCC	GTG	GAG	TGG	GAG	AGC	AAT	GGG	CAG	CCG	GAG	AAC	AAC	TAC	AAG	ACC	ACG				
I	A	V	E	W	E	S	N	G	Q	P	E	N	N	Y	K	T	T				
-----																					
1251				1260				1269				1278				1287				1296	
CCT	CCC	GTG	CTG	GAC	TCC	GAC	GGC	TCC	TTC	TTC	CTC	TAC	AGC	AAG	CTC	ACC	GTG				
P	P	V	L	D	S	D	G	S	F	F	L	Y	S	K	L	T	V				
-----																					
1305				1314				1323				1332				1341				1350	
GAC	AAG	AGC	AGG	TGG	CAG	CAG	GGG	AAC	GTC	TTC	TCA	TGC	TCC	GTG	ATG	CAT	GAG				
D	K	S	R	W	Q	Q	G	N	V	F	S	C	S	V	M	F	D				

**Fig. 12(B)**  
(Sheet 2 of 4)

1359	1368	1377	1386	1395	1404
GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCC CCG GGG AGC GGC					
A L H N H Y T Q K S L S L S P <u>G S G</u>					
1413	1422	1431	1440	1449	1458
GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG ATG TCC					
<u>G</u> L K I A A F N I Q T F G E T K M S					
1467	1476	1485	1494	1503	1512
AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC ATC GCC					
N A T L V S Y I V Q I L S R Y D I A					
1521	1530	1539	1548	1557	1566
CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG CTG GAC					
L V Q E V R D S H L T A V G K L L D					
1575	1584	1593	1602	1611	1620
AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG CCA CTG					
N L N Q D A P D T Y H Y V V S E P L					
1629	1638	1647	1656	1665	1674
GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC CAG GTG					
G R N S Y K E R Y L F V Y R P D Q V					
1683	1692	1701	1710	1719	1728
TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG AAC GAC					
S A V D S Y Y Y D D G C E P C G N D					
1737	1746	1755	1764	1773	1782
ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC TCC CGG TTC ACA GAG GTC					
T F N R E P A I V R F F S R F T E V					
1791	1800	1809	1818	1827	1836
AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA GCC GAG					
R E F A I V P L H A A P G D A V A E					
1845	1854	1863	1872	1881	1890
ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC TTG GAG					
I D A L Y D V Y L D V Q E K W G L E					
1899	1908	1917	1926	1935	1944
GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA CCC TCC					
D V M L M G D F N A G C S Y V R P S					
1953	1962	1971	1980	1989	1998
CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG ATC CCC					
Q W S S I R L W T S P T F Q W L I P					
2007	2016	2025	2034	2043	2052
GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG ATC GTG					
D S A D T T A T P T H C A Y D R I V					

**Fig. 12(B)**  
(Sheet 3 of 4)

2061	2070	2079	2088	2097	2106
GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG GCT CTT CCC TTT					
V A G M L L R G A V V P D S A L P F					
2115	2124	2133	2142	2151	2160
AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA GCC ATC AGT GAC					
N F Q A A Y G L S D Q L A Q A I S D					
2169	2178	2187	2196	2205	2214
CAC TAT CCA GTG GAG GTG ATG CTG AAG GGG GGC GGA CCC AAA AAG AAG CGC AAG					
H Y P V E V M L K G			<u>G G P K K K R K</u>		

GTT TGA 3'

-----  
V \*

***Fig. 12(B)***  
***(Sheet 4 of 4)***

## pAS101

LOCUS PAS101.DNA 1548 bp mRNA PRI 06-MAR-1995  
DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I (pAS101)  
ACCESSION  
NID  
KEYWORDS DNase I.  
SOURCE DNase I sequence is from assembled oligos (thus modified c/f  
MHDNASE1.dna)  
ORGANISM Homo sapiens  
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;  
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.  
TITLE Recombinant human DNase I reduces the viscosity of cystic  
fibrosis  
sputum  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)  
MEDLINE 91067672  
BASE COUNT 343 a 467 c 430 g 308 t  
ORIGIN

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1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGCCTCAGT GAAGGTGTCC
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241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGCACAGCGG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAAC TCA
541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAATC ACACATGCC ACCGTGCCCA GCACCTGAAG GCGGGCTGAA GATCGCAGCC
781 TTCAACATCC AGACATTTGG GGAGACCAAG ATGTCCAATG CCACCCTCGT CAGCTACATT
841 GTGCAGATCC TGAGCCGCTA CGACATCGCC CTGGTCCAGG AGGTCAGAGA CAGCCACCTG
901 ACTGCCGTGG GGAAGCTGCT GGACAACCTC AATCAGGACG CACCAGACAC CTATCACTAC
961 GTGGTCAGTG AGCCACTGGG ACGGAACAGC TATAAGGAGC GCTACCTGTT CGTGTACAGG
1021 CCTGACCAGG TGTCTGCGGT GGACAGCTAC TACTACGATG ATGGCTGCGA GCCCTGCGGG
1081 AACGACACCT TCAACCGAGA GCCAGCCATT GTCAGGTTCT TCTCCCGGTT CACAGAGGTC
1141 AGGGAGTTTG CCATTGTTCC CCTGCATGCG GCCCGGGGG ACGCAGTAGC CGAGATCGAC
1201 GCTCTCTATG ACGTCTACCT GGATGTCCAA GAGAAATGGG GCTTGAGGGA CGTCATGTTG
1261 ATGGGCGACT TCAATGCGGG CTGCAGCTAT GTGAGACCTT CCCAGTGGTC ATCCATCCGC
1321 CTGTGGACAA GCCCCACCTT CCAGTGGCTG ATCCCCGACA GCGCTGACAC CACAGCTACA
1381 CCCACGCACT GTGCCTATGA CAGGATCGTG GTTGCAAGGA TGCTGCTCCG AGGGGCCGTT
1441 GTTCCCGACT CGGCTCTTCC CTTTAACTTC CAGGCTGCCT ATGGCCTGAG TGACCAACTG
1501 GCCCAAGCCA TCAGTGACCA CTATCCAGTG GAGGTGATGC TGAAGTGA
```

//

*Fig. 13(A)*

LOCUS FDDNASE101 1548 BP SS-DNA SYN 25-AUG-2000  
 DEFINITION -  
 ACCESSION -  
 KEYWORDS -  
 SOURCE -

FEATURES Location/Qualifiers  
 frag join(1..>720,<781..1548)  
 /note="1 to 1548 of PAS101.dna [Split]"  
 frag 721..780  
 /note="1 to 60 of 101/105linker"  
 frag join(721..>735,<736..>759,<760..>780)  
 /note="1 to 80 of 102linker [Split]"

BASE COUNT 343 A 465 C 431 G 309 T 0 OTHER  
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1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCACTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGGTGTC GTGGAACCTA
541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAACTC ACACATGTCC ACCGTGTCCA GCACCAGAGG GCGGGCTGAA GATCGCAGCC
781 TTCAACATCC AGACATTTGG GGAGACCAAG ATGTCCAATG CCACCCTCGT CAGCTACATT
841 GTGCAGATCC TGAGCCGCTA CGACATCGCC CTGGTCCAGG AGGTCAGAGA CAGCCACCTG
901 ACTGCCGTGG GGAAGCTGCT GGACAACCTC AATCAGGACG CACCAGACAC CTATCACTAC
961 GTGGTCAGTG AGCCACTGGG ACGGAACAGC TATAAGGAGC GCTACCTGTT CGTGTACAGG
1021 CCTGACCAGG TGTCTGCGGT GGACAGCTAC TACTACGATG ATGGCTGCGA GCCCTGCGGG
1081 AACGACACCT TCAACCGAGA GCCAGCCATT GTCAGGTTCT TCTCCCGGTT CACAGAGGTC
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1201 GCTCTCTATG ACGTCTACCT GGATGTCCAA GAGAAATGGG GCTTGGAGGA CGTCATGTTG
1261 ATGGGCGACT TCAATGCGGG CTGCAGCTAT GTGAGACCCT CCCAGTGGTC ATCCATCCGC
1321 CTGTGGACAA GCCCCACCTT CCAGTGGCTG ATCCCCGACA GCGCTGACAC CACAGCTACA
1381 CCCACGCACT GTGCCTATGA CAGGATCGTG GTTGCAAGGA TGCTGCTCCG AGGGGCCGTT
1441 GTTCCCGACT CGGCTCTTCC CTTTAACTTC CAGGCTGCCT ATGGCCTGAG TGACCAACTG
1501 GCCCAAGCCA TCAGTGACCA CTATCCAGTG GAGGTGATGC TGAAGTGA

```

//

**Fig. 13(B)**

LOCUS FDDNASE101 1557 BP SS-DNA SYN 29-AUG-2000

DEFINITION -

ACCESSION -

KEYWORDS -

SOURCE -

FEATURES Location/Qualifiers

frag 10..1557

/note="1 to 1548 of FdDNase101correct"

frag join(10..>729,<790..1557)

/note="1 to 1548 of PAS101.dna [Split]"

frag 730..789

/note="1 to 60 of 101/105linker"

frag join(730..>744,<745..>768,<769..>789)

/note="1 to 80 of 102linker [Split]"

BASE COUNT 344 A 471 C 433 G 309 T 0 OTHER

ORIGIN -

1 GCCGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTGTC

61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG

121 AAGGTGTCCT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC

181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATTT TACCTGGAAG TAATAATTCT

241 AGATAACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA

301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA

361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA

421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCCT CCTCCAAGAG CACCTCTGGG

481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCAGG GACGGTGTCG

541 TGGAACCTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA

601 GGAATCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC

661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC

721 AAATCTTGTTG ACAAACCTCA CACATGTCCA CCGTGTCCAG CACCAGAGGG CGGGCTGAAG

781 ATCGCAGCCT TCAACATCCA GACATTTGGG GAGACCAAGA TGTCCAATGC CACCCTCGTC

841 AGCTACATTG TGCAGATCCT GAGCCGCTAC GACATCGCCC TGGTCCAGGA GGTGAGAGAC

901 AGCCACCTGA CTGCCGTGGG GAAGCTGCTG GACAACCTCA ATCAGGACGC ACCAGACACC

961 TATCACTACG TGGTCAGTGA GCCACTGGGA CGGAACAGCT ATAAGGAGCG CTACCTGTTC

1021 GTGTACAGGC CTGACCAGGT GTCTGCGGTG GACAGCTACT ACTACGATGA TGGCTGCGAG

1081 CCCTGCGGGA ACGACACCTT CAACCGAGAG CCAGCCATTG TCAGGTTCTT CTCCCGGTTT

1141 ACAGAGGTCA GGGAGTTTGC CATTGTTCCC CTGCATGCGG CCCCAGGGGA CGCAGTAGCC

1201 GAGATCGACG CTCTCTATGA CGTCTACCTG GATGTCCAAG AGAAATGGGG CTTGGAGGAC

1261 GTCATGTTGA TGGGCGACTT CAATGCGGGC TGCAGCTATG TGAGACCCTC CCAGTGGTCA

1321 TCCATCCGCC TGTGGACAAG CCCCACCTTC CAGTGGCTGA TCCCCGACAG CGCTGACACC

1381 ACAGCTACAC CCACGCACTG TGCTATGAC AGGATCGTGG TTGCAGGGAT GCTGCTCCGA

1441 GGGGCCGTTG TTCCCGACTC GGCTCTTCCC TTAACTTCC AGGCTGCCTA TGGCCTGAGT

1501 GACCAACTGG CCCAAGCCAT CAGTGACCAC TATCCAGTGG AGGTGATGCT GAAGTGA

//

**Fig. 13(C)**

5'	ATG	GGA	TGG	AGC	TGT	ATC	ATC	CTC	TTC	TTG	GTA	GCA	ACA	GCT	ACA	GGT	GTC	CAC
	M	G	W	S	C	I	I	L	F	L	V	A	T	A	T	G	V	H
	TCC	CAG	GTG	CAG	CTG	GTG	CAG	TCT	GGG	GCA	GAG	GTG	AAA	AAG	CCT	GGG	GCC	TCA
	S	Q	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	A	S
	GTG	AAG	GTG	TCC	TGC	AAG	GCT	TCT	GGC	TAC	ACC	TTC	AGT	GCC	TAC	TGG	ATA	GAG
	V	K	V	S	C	K	A	S	G	Y	T	F	S	A	Y	W	I	E
	TGG	GTG	CGC	CAG	GCT	CCA	GGA	AAG	GGC	CTC	GAG	TGG	GTC	GGA	GAG	ATT	TTA	CCT
	W	V	R	Q	A	P	G	K	G	L	E	W	V	G	E	I	L	P
	GGA	AGT	AAT	AAT	TCT	AGA	TAC	AAT	GAG	AAG	TTC	AAG	GGC	CGA	GTG	ACA	GTC	ACT
	G	S	N	N	S	R	Y	N	E	K	F	K	G	R	V	T	V	T
	AGA	GAC	ACA	TCC	ACA	AAC	ACA	GCC	TAC	ATG	GAG	CTC	AGC	AGC	CTG	AGG	TCT	GAG
	R	D	T	S	T	N	T	A	Y	M	E	L	S	S	L	R	S	E
	GAC	ACA	GCC	GTC	TAT	TAC	TGT	GCA	AGA	TCC	TAC	GAC	TTT	GCC	TGG	TTT	GCT	TAC
	D	T	A	V	Y	Y	C	A	R	S	Y	D	F	A	W	F	A	Y
	TGG	GGC	CAA	GGG	ACT	CTG	GTC	ACA	GTC	TCC	TCA	GCC	TCC	ACC	AAG	GGC	CCA	TCG
	W	G	Q	G	T	L	V	T	V	S	S	A	S	T	K	G	P	S
	GTC	TTC	CCC	CTG	GCA	CCC	TCC	TCC	AAG	AGC	ACC	TCT	GGG	GGC	ACA	GCG	GCC	CTG
	V	F	P	L	A	P	S	S	K	S	T	S	G	G	T	A	A	L
	GGC	TGC	CTG	GTC	AAG	GAC	TAC	TTC	CCC	GAA	CCG	GTG	ACG	GTG	TCG	TGG	AAC	TCA
	G	C	L	V	K	D	Y	F	P	E	P	V	T	V	S	W	N	S
	GGC	GCC	CTG	ACC	AGC	GGC	GTG	CAC	ACC	TTC	CCG	GCT	GTC	CTA	CAG	TCC	TCA	GGA
	G	A	L	T	S	G	V	H	T	F	P	A	V	L	Q	S	S	G

**Fig. 13(D)**  
(Sheet 1 of 3)





GCC	GAG	ATC	GAC	GCT	CTC	TAT	GAC	GTC	TAC	CTG	GAT	GTC	CAA	GAG	AAA	TGG	GGC						
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---						
A	E	I	D	A	L	Y	D	V	Y	L	D	V	Q	E	K	W	G						
1251				1260				1269				1278				1287				1296			
TTG	GAG	GAC	GTC	ATG	TTG	ATG	GGC	GAC	TTC	AAT	GCG	GGC	TGC	AGC	TAT	GTG	AGA						
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---						
L	E	D	V	M	L	M	G	D	F	N	A	G	C	S	Y	V	R						
1305				1314				1323				1332				1341				1350			
CCC	TCC	CAG	TGG	TCA	TCC	ATC	CGC	CTG	TGG	ACA	AGC	CCC	ACC	TTC	CAG	TGG	CTG						
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---						
P	S	Q	W	S	S	I	R	L	W	T	S	P	T	F	Q	W	L						
1359				1368				1377				1386				1395				1404			
ATC	CCC	GAC	AGC	GCT	GAC	ACC	ACA	GCT	ACA	CCC	ACG	CAC	TGT	GCC	TAT	GAC	AGG						
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---						
I	P	D	S	A	D	T	T	A	T	P	T	H	C	A	Y	D	R						
1413				1422				1431				1440				1449				1458			
ATC	GTG	GTT	GCA	GGG	ATG	CTG	CTC	CGA	GGG	GCC	GTT	GTT	CCC	GAC	TCG	GCT	CTT						
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---						
I	V	V	A	G	M	L	L	R	G	A	V	V	P	D	S	A	L						
1467				1476				1485				1494				1503				1512			
CCC	TTT	AAC	TTC	CAG	GCT	GCC	TAT	GGC	CTG	AGT	GAC	CAA	CTG	GCC	CAA	GCC	ATC						
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---						
P	F	N	F	Q	A	A	Y	G	L	S	D	Q	L	A	Q	A	I						
1521				1530				1539				1548											
AGT	GAC	CAC	TAT	CCA	GTG	GAG	GTG	ATG	CTG	AAG	TGA	3'											
---	---	---	---	---	---	---	---	---	---	---	---	---											
S	D	H	Y	P	V	E	V	M	L	K	*												

**Fig. 13(D)**  
**(Sheet 3 of 3)**

## pAS102

LOCUS PAS102.DNA 1566 bp mRNA PRI 06-MAR-1995  
 DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I (pAS102)  
 ACCESSION  
 NID  
 KEYWORDS DNase I.  
 SOURCE DNase I sequence is from assembled oligos (thus modified c/f  
 MHDNASE1.dna) (See Figure 2)  
 ORGANISM Homo sapiens  
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;  
 Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 AUTHORS Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.  
 TITLE Recombinant human DNase I reduces the viscosity of cystic  
 fibrosis  
 sputum  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)  
 MEDLINE 91067672  
 BASE COUNT 345 a 469 c 440 g 312 t  
 ORIGIN

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1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
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301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTIONTC CCCGAACCGG TGACGGGTGTC GTGGAAGTCA
541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAATC ACACATGCTG TGTGGAGTGC CCACCGTGCC CAGCACCTGA AGGGAGCGGC
781 GGGCTGAAGA TCGCAGCCTT CAACATCCAG ACATTTGGGG AGACCAAGAT GTCCAATGCC
841 ACCCTCGTCA GCTACATTGT GCAGATCCTG AGCCGCTACG ACATCGCCCT GGTCCAGGAG
901 GTCAGAGACA GCCACCTGAC TGCCGTGGGG AAGCTGCTGG ACAACCTCAA TCAGGACGCA
961 CCAGACACCT ATCACTACGT GGTCAGTGAG CCACTGGGAC GGAACAGCTA TAAGGAGCGC
1021 TACCTGTTCTG TGTACAGGCC TGACCAGGTG TCTGCGGTGG ACAGCTACTA CTACGATGAT
1081 GGCTGCGAGC CCTGCGGGAA CGACACCTTC AACCAGAGAG CAGCCATTGT CAGGTTCTTC
1141 TCCCGGTTC CAGAGGTCAG GGAGTTTGCC ATTGTTCCCC TGCATGCGGC CCCGGGGGAC
1201 GCAGTAGCCG AGATCGACGC TCTCTATGAC GTCTACCTGG ATGTCCAAGA GAAATGGGGC
1261 TTGGAGGACG TCATGTTGAT GGGCGACTTC AATGCGGGCT GCAGCTATGT GAGACCTTCC
1321 CAGTGCTCAT CCATCCGCCT GTGGACAAGC CCCACCTTCC AGTGGCTGAT CCCCGACAGC
1381 GCTGACACCA CAGCTACACC CACGCACTGT GCCTATGACA GGATCGTGGT TGCAGGGATG
1441 CTGCTCCGAG GGGCCGTTGT TCCCGACTCG GCTCTTCCCT TTAAGTTCCA GGCTGCCTAT
1501 GGCCTGAGTG ACCAACTGGC CCAAGCCATC AGTGACCACT ATCCAGTGGA GGTGATGCTG
1561 AAGTGA

```

//

**Fig. 14(A)**

LOCUS FDDNASE102 1566 BP SS-DNA SYN 23-MAR-2001  
 DEFINITION -  
 ACCESSION -  
 KEYWORDS -  
 SOURCE -  
 BASE COUNT 345 A 468 C 440 G 313 T 0 OTHER  
 ORIGIN -

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG  
 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC  
 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA  
 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT  
 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG  
 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC  
 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC  
 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG  
 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAAC TCA  
 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC  
 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC  
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 841 ACCCTCGTCA GCTACATTGT GCAGATCCTG AGCCGCTACG ACATCGCCCT GTTCCAGGAG  
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 1321 CAGTGGTCAT CCATCCGCCT GTGGACAAGC CCCACCTTCC AGTGGCTGAT CCCCAGACAGC  
 1381 GCTGACACCA CAGCTACACC CACGCACTGT GCCTATGACA GGATCGTGGT TGCAGGGATG  
 1441 CTGCTCCGAG GGGCCGTTGT TCCCGACTCG GCTCTTCCCT TTAACCTCCA GGCTGCCTAT  
 1501 GGCTGAGTG ACCAACTGGC CCAAGCCATC AGTGACCACT ATCCAGTGGA GGTGATGCTG  
 1561 AAGTGA

//

**Fig. 14(B)**

## pAS302

LOCUS FDDNASE302 1575 BP SS-DNA SYN 29-AUG-2000  
DEFINITION -  
ACCESSION -  
KEYWORDS -  
SOURCE -

FEATURES Location/Qualifiers  
frag 10..1575  
/note="1 to 1566 of FdDNase102correct"

BASE COUNT 346 A 474 C 442 G 313 T 0 OTHER  
ORIGIN -

1 GCCGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTGTC  
61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG  
121 AAGGTGTCCT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC  
181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATTT TACCTGGAAG TAATAATTCT  
241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA  
301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA  
361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA  
421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCCT CCTCCAAGAG CACCTCTGGG  
481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTCTG  
541 TGGAACTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCTT ACAGTCCTCA  
601 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC  
661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC  
721 AAATCTTG TG ACAA AACTCA CACATGCTGT GTCGAGTGTC CACCGTGTCC AGCACCAGAG  
781 GGGAGCGGCG GGCTGAAGAT CGCAGCCTTC AACATCCAGA CATTTGGGGA GACCAAGATG  
841 TCCAATGCCA CCCTCGTCAG CTACATTGTG CAGATCCTGA GCCGCTACGA CATCGCCCTG  
901 GTCCAGGAGG TCAGAGACAG CCACCTGACT GCCGTGGGGA AGCTGCTGGA CAACCTCAAT  
961 CAGGACGCAC CAGACACCTA TCACTACGTG GTCAGTGAGC CACTGGGACG GAACAGCTAT  
1021 AAGGAGCGCT ACCTGTTCTG GTACAGGCCT GACCAGGTGT CTGCGGTGGA CAGCTACTAC  
1081 TACGATGATG GCTGCGAGCC CTGCGGGAAC GACACCTTCA ACCGAGAGCC AGCCATTGTC  
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1261 AAATGGGGCT TGGAGGACGT CATGTTGATG GGCGACTTCA ATGCGGGCTG CAGCTATGTG  
1321 AGACCTCCC AGTGGTCATC CATCCGCCTG TGGACAAGCC CCACCTTCCA GTGGCTGATC  
1381 CCCGACAGCG CTGACACCAC AGCTACACCC ACGCACTGTG CCTATGACAG GATCGTGGTT  
1441 GCAGGGATGC TGCTCCGAGG GGCCGTTGTT CCCGACTCGG CTCTTCCCTT TAACTTCCAG  
1501 GCTGCCTATG GCCTGAGTGA CCAACTGGCC CAAGCCATCA GTGACCACTA TCCAGTGGAG  
1561 GTGATGCTGA AGTGA

//

*Fig. 14(C)*

9	18	27	36	45	54
ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC					
M G W S C I I L F L V A T A T G V H					
63	72	81	90	99	108
TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA					
S Q V Q L V Q S G A E V K K P G A S					
117	126	135	144	153	162
GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG					
V K V S C K A S G Y T F S A Y W I E					
171	180	189	198	207	216
TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT					
W V R Q A P G K G L E W V G E I L P					
225	234	243	252	261	270
GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT					
G S N N S R Y N E K F K G R V T V T					
279	288	297	306	315	324
AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG					
R D T S T N T A Y M E L S S L R S E					
333	342	351	360	369	378
GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC					
D T A V Y Y C A R S Y D F A W F A Y					
387	396	405	414	423	432
TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG					
W G Q G T L V T V S S A S T K G P S					
441	450	459	468	477	486
GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG					
V F P L A P S S K S T S G G T A A L					
495	504	513	522	531	540
GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA					
G C L V K D Y F P E P V T V S W N S					
549	558	567	576	585	594
GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA					
G A L T S G V H T F P A V L Q S S G					

**Fig. 14(D)**  
(Sheet 1 of 3)

603	612	621	630	639	648
CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG					
L Y S L S S V V T V P S S S L G T Q					
657	666	675	684	693	702
ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA					
T Y I C N V N H K P S N T K V D K K					
711	720	729	738	747	756
GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC TGT GTG GAG TGC CCA CCG					
V E P K S C D K T H T C C V E C P P					
765	774	783	792	801	810
TGC CCA GCA CCT GAA GGG AGC GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG					
C P A P E G S G G L K I A A F N I Q					
819	828	837	846	855	864
ACA TTT GGG GAG ACC AAG ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG					
T F G E T K M S N A T L V S Y I V Q					
873	882	891	900	909	918
ATC CTG AGC CGC TAC GAC ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG					
I L S R Y D I A L V Q E V R D S H L					
927	936	945	954	963	972
ACT GCC GTG GGG AAG CTG CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT					
T A V G K L L D N L N Q D A P D T Y					
981	990	999	1008	1017	1026
CAC TAC GTG GTC AGT GAG CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG					
H Y V V S E P L G R N S Y K E R Y L					
1035	1044	1053	1062	1071	1080
TTC GTG TAC AGG CCT GAC CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT					
F V Y R P D Q V S A V D S Y Y Y D D					
1089	1098	1107	1116	1125	1134
GGC TGC GAG CCC TGC GGG AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG					
G C E P C G N D T F N R E P A I V R					
1143	1152	1161	1170	1179	1188
TTC TTC TCC CGG TTC ACA GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG					
F F S R F T E V R E F A I V P L H A					
1197	1206	1215	1224	1233	1242

**Fig. 14(D)**  
(Sheet 2 of 3)



## pAS103

LOCUS PAS103.DNA 1560 bp mRNA PRI 06-MAR-1995  
DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I (pAS103)  
ACCESSION  
NID  
KEYWORDS DNase I.  
SOURCE DNase I sequence is from assembled oligos (thus modified c/f  
MHDNASE1.dna)  
ORGANISM Homo sapiens  
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;  
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.  
TITLE Recombinant human DNase I reduces the viscosity of cystic  
fibrosis  
sputum  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)  
MEDLINE 91067672  
BASE COUNT 344 a 468 c 436 g 312 t  
ORIGIN

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1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCACTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGA TACTTTC CCCGAACCGG TGACGGTGTC GTGGA ACTCA
541 GCGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAATC ACACATGCTG TGTGGAGTGC CCACCGTGCC CAGCACCTGA AGGCGGGCTG
781 AAGATCGCAG CCTTCAACAT CCAGACATTT GGGGAGACCA AGATGTCCAA TGCCACCCCTC
841 GTCAGCTACA TTGTGCAGAT CCTGAGCCGC TACGACATCG CCCTGGTCCA GGAGGTCAGA
901 GACAGCCACC TGA CTGCCGT GGGGAAGCTG CTGGACAACC TCAATCAGGA CGCACCAGAC
961 ACCTATCACT ACGTGGTCAG TGAGCCACTG GGACGGAACA GCTATAAGGA GCGCTACCTG
1021 TTCGTGTACA GGCCTGACCA GGTGTCTGCG GTGGACAGCT ACTACTACGA TGATGGCTGC
1081 GAGCCCTGCG GGAACGACAC CTTCAACCGA GAGCCAGCCA TTGTCAGGTT CTTCTCCCGG
1141 TTCACAGAGG TCAGGGAGTT TGCCATTGTT CCCCTGCATG CGGCCCCGGG GGACGCAGTA
1201 GCCGAGATCG ACGCTCTCTA TGACGTCTAC CTGGATGTCC AAGAGAAATG GGGCTTGGAG
1261 GACGTCATGT TGATGGGCGA CTTCAATGCG GGCTGCAGCT ATGTGAGACC CTCCCAGTGG
1321 TCATCCATCC GCCTGTGGAC AAGCCCCACC TTCCAGTGGC TGATCCCCGA CAGCGCTGAC
1381 ACCACAGCTA CACCCACGCA CTGTGCCTAT GACAGGATCG TGGTTGCAGG GATGCTGCTC
1441 CGAGGGGCCG TTGTTCCCGA CTCGGCTCTT CCCTTTAACT TCCAGGCTGC CTATGGCCTG
1501 AGTGACCAAC TGGCCCAAGC CATCAGTGAC CACTATCCAG TGGAGGTGAT GCTGAAGTGA
```

//

*Fig. 15(A)*



LOCUS FDDNASE103 1560 BP SS-DNA SYN 25-AUG-2000

DEFINITION -

ACCESSION -

KEYWORDS -

SOURCE -

FEATURES

Location/Qualifiers

frag join(1..>720,<793..1560)

/note="1 to 1560 of PAS103.dna [Split]"

frag 721..792

/note="1 to 72 of 103/107linker"

frag join(721..>771,<772..792)

/note="1 to 78 of 102linker [Split]"

BASE COUNT 344 A 467 C 436 G 313 T 0 OTHER

ORIGIN

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG

61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC

121 TGCAAGGCTT CTGGCTACAC CTTCAAGTCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA

181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT

241 GAGAAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG

301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC

361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC

421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG

481 GCCCTGGGCT GCCTGGTCAA GGAATACTTC CCCGAACCGG TGACGGTGTC GTGGAATCA

541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCTC AGGACTCTAC

601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC

661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT

721 GACAAAATC ACACATGCTG TGTCGAGTGT CCACCGTGTC CAGCACCAGA GGGCGGGCTG

781 AAGATCGCAG CCTTCAACAT CCAGACATTT GGGGAGACCA AGATGTCCAA TGCCACCCTC

841 GTCAGCTACA TTGTGCAGAT CCTGAGCCGC TACGACATCG CCCTGGTCCA GGAGGTCAGA

901 GACAGCCACC TGAAGTCCGT GGGGAAGCTG CTGGACAACC TCAATCAGGA CGCACCAGAC

961 ACCTATCACT ACGTGGTCAG TGAGCCACTG GGACGGAACA GCTATAAGGA GCGCTACCTG

1021 TTCGTGTACA GGCCTGACCA GGTGTCTGCG GTGGACAGCT ACTACTACGA TGATGGCTGC

1081 GAGCCCTGCG GGAACGACAC CTTCAACCGA GAGCCAGCCA TTGTCAGGTT CTTCTCCCGG

1141 TTCACAGAGG TCAGGGAGTT TGCCATTGTT CCCCTGCATG CGGCCCCGGG GGACGCAGTA

1201 GCCGAGATCG ACGCTCTCTA TGACGTCTAC CTGGATGTCC AAGAGAAATG GGGCTTGGAG

1261 GACGTCAATG TGATGGGCGA CTTCAATGCG GGCTGCAGCT ATGTGAGACC CTCCCAGTGG

1321 TCATCCATCC GCCTGTGGAC AAGCCCCACC TTCCAGTGGC TGATCCCCGA CAGCGCTGAC

1381 ACCACAGCTA CACCCACGCA CTGTGCCTAT GACAGGATCG TGGTTGCAGG GATGCTGCTC

1441 CGAGGGGCGG TTGTTCCCGA CTCGGCTCTT CCCTTTAACT TCCAGGCTGC CTATGGCCTG

1501 AGTGACCAAC TGGCCCAAGC CATCAGTGAC CACTATCCAG TGGAGGTGAT GCTGAAGTGA

//

**Fig. 15(B)**

LOCUS FDDNASE103 1569 BP SS-DNA SYN 29-AUG-2000

DEFINITION -

ACCESSION -

KEYWORDS -

SOURCE -

FEATURES

frag 10..1569

frag join(10..>729,<802..1569)

frag 730..801

frag join(730..>780,<781..801)

BASE COUNT 345 A 473 C 438 G 313 T 0 OTHER

ORIGIN

1 GCCGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTGTC

61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG

121 AAGGTGTCCT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC

181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATTT TACCTGGAAG TAATAATTCT

241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA

301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA

361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA

421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCCT CCTCCAAGAG CACCTCTGGG

481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTGCG

541 TGGAACCTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA

601 GGAATCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC

661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC

721 AAATCTTG TG ACAAACCTCA CACATGCTGT GTCGAGTGTC CACCGTGTCC AGCACCAGAG

781 GGC GGGCTGA AGATCGCAGC CTTCAACATC CAGACATTTG GGGAGACCAA GATGTCCAAT

841 GCCACCCTCG TCAGCTACAT TGTGCAGATC CTGAGCCGCT ACGACATCGC CCTGGTCCAG

901 GAGGTCAGAG ACAGCCACCT GACTGCCGTG GGGAAGCTGC TGGACAACCT CAATCAGGAC

961 GCACCAGACA CCTATCACTA CGTGCTCAGT GAGCCACTGG GACGGAACAG CTATAAGGAG

1021 CGCTACCTGT TCGTGTACAG GCCTGACCAG GTGTCTGCGG TGGACAGCTA CTACTACGAT

1081 GATGGCTGCG AGCCCTGCGG GAACGACACC TTCAACCGAG AGCCAGCCAT TGTCAGGTTC

1141 TTCTCCCGGT TCACAGAGGT CAGGGAGTTT GCCATTGTTT CCCTGCATGC GGCCCCGGGG

1201 GACGCAGTAG CCGAGATCGA CGCTCTCTAT GACGTCTACC TGGATGTCCA AGAGAAATGG

1261 GGCTTGGAGG ACGTCATGTT GATGGGCGAC TTCAATGCGG GCTGCAGCTA TGTGAGACCC

1321 TCCCAGTGGT CATCCATCCG CCTGTGGACA AGCCCCACCT TCCAGTGGCT GATCCCCGAC

1381 AGCGCTGACA CCACAGCTAC ACCCACGCAC TGTGCCTATG ACAGGATCGT GGTTCAGGG

1441 ATGCTGCTCC GAGGGGCGGT TGTTCCTGAC TCGGCTCTTC CCTTTAACTT CCAGGCTGCC

1501 TATGGCCTGA GTGACCAACT GGCCCAAGCC ATCAGTGACC ACTATCCAGT GGAGGTGATG

1561 CTGAAGTGA

//

**Fig. 15(C)**



603	612	621	630	639	648
CTC TAC TCC CTC AGC	AGC GTG GTG ACC GTG CCC	TCC AGC AGC TTG GGC	ACC CAG		
---	---	---	---	---	---
L Y S L S S V V T V P S S S L G T Q					
657	666	675	684	693	702
ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA					
---	---	---	---	---	---
T Y I C N V N H K P S N T K V D F K					
711	720	729	738	747	756
GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC TGT GTG GAG TGC CCA CCG					
---	---	---	---	---	---
V E P K S C D K T H T C C V E C P P					
765	774	783	792	801	810
TGC CCA GCA CCT GAA GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT					
---	---	---	---	---	---
C P A P E G G L K I A A F N I Q T F					
819	828	837	846	855	864
GGG GAG ACC AAG ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG					
---	---	---	---	---	---
G E T K M S N A T L V S Y I V Q I L					
873	882	891	900	909	918
AGC CGC TAC GAC ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC					
---	---	---	---	---	---
S R Y D I A L V Q E V R D S H L T A					
927	936	945	954	963	972
GTG GGG AAG CTG CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC					
---	---	---	---	---	---
V G K L L D N L N Q D A P D T Y H Y					
981	990	999	1008	1017	1026
GTG GTC AGT GAG CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG					
---	---	---	---	---	---
V V S E P L G R N S Y K E R Y L F V					
1035	1044	1053	1062	1071	1080
TAC AGG CCT GAC CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC					
---	---	---	---	---	---
Y R P D Q V S A V D S Y Y Y D D G C					
1089	1098	1107	1116	1125	1134
GAG CCC TGC GGG AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC					
---	---	---	---	---	---
E P C G N D T F N R E P A I V R F F					
1143	1152	1161	1170	1179	1188
TCC CGG TTC ACA GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG					
---	---	---	---	---	---
S R F T E V R E F A I V P L H A A P					
1197	1206	1215	1224	1233	1242

**Fig. 15(D)**  
**(Sheet 2 of 3)**



## pAS104

LOCUS PAS104.DNA 1560 bp mRNA PRI 06-MAR-1995  
DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I (pAS104)  
Position 924 G to A by ggg to gag  
Linker GR instead of GG (position 777)  
ACCESSION  
NID  
KEYWORDS DNase I.  
SOURCE DNase I sequence is from assembled oligos (thus modified c/f  
MHDNASE1.dna)  
ORGANISM Homo sapiens  
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;  
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.  
TITLE Recombinant human DNase I reduces the viscosity of cystic  
fibrosis  
sputum  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)  
MEDLINE 91067672  
BASE COUNT 346 a 468 c 434 g 312 t  
ORIGIN

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1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAGGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTIONC CCCGAACCGG TGACGGTGTC GTGGAACCTA
541 GCGGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAACCTC ACACATGCTG TGTGGAGTGC CCACCGTGCC CAGCACCTGA AGGCAGGCTG
781 AAGATCGCAG CCTTCAACAT CCAGACATTT GGGGAGACCA AGATGTCCAA TGCCACCCTC
841 GTCAGCTACA TTGTGCAGAT CCTGAGCCGC TACGACATCG CCCTGGTCCA GGAGGTCAGA
901 GACAGCCACC TGAATGCCGT GGAGAAGCTG CTGGACAACC TCAATCAGGA CGCACCAGAC
961 ACCTATCACT ACGTGGTCAG TGAGCCACTG GGACGGAACA GCTATAAGGA GCGCTACCTG
1021 TTCGTGTACA GGCCTGACCA GGTGTCTGCG GTGGACAGCT ACTACTACGA TGATGGCTGC
1081 GAGCCCTGCG GGAACGACAC CTTCAACCGA GAGCCAGCCA TTGTGAGGTT CTTCTCCCGG
1141 TTCACAGAGG TCAGGGAGTT TGCCATTGTT CCCCTGCATG CGGCCCCGGG GGACGCAGTA
1201 GCCGAGATCG ACGCTCTCTA TGACGTCTAC CTGGATGTCC AAGAGAAATG GGGCTTGGAG
1261 GACGTCATGT TGATGGGCGA CTTCAATGCG GGCTGCAGCT ATGTGAGACC CTCCAGTGG
1321 TCATCCATCC GCCTGTGGAC AAGCCCCACC TTCCAGTGGC TGATCCCCGA CAGCGCTGAC
1381 ACCACAGCTA CACCCACGCA CTGTGCCTAT GACAGGATCG TGGTTGCAGG GATGCTGCTC
1441 CGAGGGGCGG TTGTTCCCGA CTCGGCTCTT CCTTTAACT TCCAGGCTGC CTATGGCCTG
1501 AGTGACCAAC TGGCCCAAGC CATCAGTGAC CACTATCCAG TGGAGGTGAT GCTGAAGTGA
```

//

*Fig. 16(A)*

LOCUS FDDNASE104 1560 BP SS-DNA SYN 25-AUG-2000  
 DEFINITION -  
 ACCESSION -  
 KEYWORDS -  
 SOURCE -

FEATURES Location/Qualifiers  
 frag join(1..>720,<793..1560)  
 /note="1 to 1560 of PAS104.dna [Split]"  
 frag 721..792  
 /note="1 to 72 of 104linker"  
 frag join(721..>774,<776..792)  
 /note="1 to 72 of 103linker [Split]"  
 frag join(721..>771,<772..>774,<776..792)  
 /note="1 to 78 of 102linker [Split]"

BASE COUNT 346 A 467 C 434 G 313 T 0 OTHER

ORIGIN -  
 1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG  
 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC  
 121 TGCAAGGCTT CTGGCTACAC CTTCACTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA  
 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATAACAAT  
 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG  
 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC  
 361 TTTGCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC  
 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG  
 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACCTCA  
 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC  
 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC  
 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT  
 721 GACAAAATC ACACATGCTG TGTCGAGTGT CCACCGTGTC CAGCACCAGA GGGCAGGCTG  
 781 AAGATCGCAG CCTTCAACAT CCAGACATTT GGGGAGACCA AGATGTCCAA TGCCACCCTC  
 841 GTCAGCTACA TTGTGCAGAT CCTGAGCCGC TACGACATCG CCCTGGTCCA GGAGGTCAGA  
 901 GACAGCCACC TGA CTGCGGT GGAGAAGCTG CTGGACAACC TCAATCAGGA CGCACCAGAC  
 961 ACCTATCACT ACGTGGTCAG TGAGCCACTG GGACGGAACA GCTATAAGGA GCGCTACCTG  
 1021 TTCGTGTACA GGCCTGACCA GGTGTCTGCG GTGGACAGCT ACTACTACGA TGATGGCTGC  
 1081 GAGCCCTGCG GGAACGACAC CTTCAACCGA GAGCCAGCCA TTGTCAGGTT CTTCTCCCGG  
 1141 TTCACAGAGG TCAGGGAGTT TGCCATTGTT CCCCTGCATG CGGCCCCGGG GGACGCAGTA  
 1201 GCCGAGATCG ACGTCTCTA TGACGTCTAC CTGGATGTCC AAGAGAAATG GGGCTTGGAG  
 1261 GACGTCATGT TGATGGGCGA CTTCAATGCG GGCTGCAGCT ATGTGAGACC CTCCCAGTGG  
 1321 TCATCCATCC GCCTGTGGAC AAGCCCCACC TTCCAGTGGC TGATCCCCGA CAGCGCTGAC  
 1381 ACCACAGCTA CACCCACGCA CTGTGCCTAT GACAGGATCG TGGTTGCAGG GATGCTGCTC  
 1441 CGAGGGGCCG TTGTTCCCGA CTCGGCTCTT CCCTTTAACT TCCAGGCTGC CTATGGCCTG  
 1501 AGTGACCAAC TGGCCCAAGC CATCAGTGAC CACTATCCAG TGGAGGTGAT GCTGAAGTGA

//

**Fig. 16(B)**

5'		9		18		27		36		45		54						
	ATG	GGA	TGG	AGC	TGT	ATC	ATC	CTC	TTC	TTG	GTA	GCA	ACA	GCT	ACA	GGT	GTC	CAC
	M	G	W	S	C	I	I	L	F	L	V	A	T	A	T	G	V	P
		63		72		81		90		99		108						
	TCC	CAG	GTG	CAG	CTG	GTG	CAG	TCT	GGG	GCA	GAG	GTG	AAA	AAG	CCT	GGG	GCC	TCA
	S	Q	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	A	S
		117		126		135		144		153		162						
	GTG	AAG	GTG	TCC	TGC	AAG	GCT	TCT	GGC	TAC	ACC	TTC	AGT	GCC	TAC	TGG	ATA	GAG
	V	K	V	S	C	K	A	S	G	Y	T	F	S	A	Y	W	I	E
		171		180		189		198		207		216						
	TGG	GTG	CGC	CAG	GCT	CCA	GGA	AAG	GGC	CTC	GAG	TGG	GTC	GGA	GAG	ATT	TTA	CCT
	W	V	R	Q	A	P	G	K	G	L	E	W	V	G	E	I	L	P
		225		234		243		252		261		270						
	GGA	AGT	AAT	AAT	TCT	AGA	TAC	AAT	GAG	AAG	TTC	AAG	GGC	CGA	GTG	ACA	GTC	ACT
	G	S	N	N	S	R	Y	N	E	K	F	K	G	R	V	T	V	T
		279		288		297		306		315		324						
	AGA	GAC	ACA	TCC	ACA	AAC	ACA	GCC	TAC	ATG	GAG	CTC	AGC	AGC	CTG	AGG	TCT	GAG
	R	D	T	S	T	N	T	A	Y	M	E	L	S	S	L	R	S	E
		333		342		351		360		369		378						
	GAC	ACA	GCC	GTC	TAT	TAC	TGT	GCA	AGA	TCC	TAC	GAC	TTT	GCC	TGG	TTT	GCT	TAC
	D	T	A	V	Y	Y	C	A	R	S	Y	D	F	A	W	F	A	Y
		387		396		405		414		423		432						
	TGG	GGC	CAA	GGG	ACT	CTG	GTC	ACA	GTC	TCC	TCA	GCC	TCC	ACC	AAG	GGC	CCA	TGG
	W	G	Q	G	T	L	V	T	V	S	S	A	S	T	K	G	P	S
		441		450		459		468		477		486						
	GTC	TTC	CCC	CTG	GCA	CCC	TCC	TCC	AAG	AGC	ACC	TCT	GGG	GGC	ACA	GCG	GCC	CTG
	V	F	P	L	A	P	S	S	K	S	T	S	G	G	T	A	A	L
		495		504		513		522		531		540						
	GGC	TGC	CTG	GTC	AAG	GAC	TAC	TTC	CCC	GAA	CCG	GTG	ACG	GTG	TGG	TGG	AAC	TCA
	G	C	L	V	K	D	Y	F	P	E	P	V	T	V	S	W	N	S
		549		558		567		576		585		594						
	GGC	GCC	CTG	ACC	AGC	GGC	GTG	CAC	ACC	TTC	CCG	GCT	GTC	CTA	CAG	TCC	TCA	GGA
	G	A	L	T	S	G	V	H	T	F	P	A	V	L	Q	S	S	G

**Fig. 16(C)**  
(Sheet 1 of 3)







## pAS105

LOCUS PAS105.DNA 1578 bp mRNA PRI 06-MAR-1995  
 DEFINITION Humanised HMEG1 Fab'2 fused to human DNase I with SV40  
 NLS (pAS105)  
 ACCESSION  
 NID  
 KEYWORDS DNase I.  
 SOURCE DNase I sequence is from assembled oligos (thus modified c/f  
 MHDNASE1.dna)  
 ORGANISM Homo sapiens  
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;  
 Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 AUTHORS Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.  
 TITLE Recombinant human DNase I reduces the viscosity of cystic  
 fibrosis  
 sputum  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)  
 MEDLINE 91067672  
 BASE COUNT 353 a 473 c 442 g 310 t  
 ORIGIN

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1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAAGTCA
541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAACTC ACACATGCCC ACCGTGCCCA GCACCTGAAG GCGGGCTGAA GATCGCAGCC
781 TTCAACATCC AGACATTTGG GGAGACCAAG ATGTCCAATG CCACCCTCGT CAGCTACATT
841 GTGCAGATCC TGAGCCGCTA CGACATCGCC CTGGTCCAGG AGGTCAGAGA CAGCCACCTG
901 ACTGCCGTGG GGAAGCTGCT GGACAACCTC AATCAGGACG CACCAGACAC CTATCACTAC
961 GTGGTCAGTG AGCCACTGGG ACGGAACAGC TATAAGGAGC GCTACCTGTT CGTGTACAGG
1021 CCTGACCAGG TGTCTGCGGT GGACAGCTAC TACTACGATG ATGGCTGCGA GCCCTGCGGG
1081 AACGACACCT TCAACCGAGA GCCAGCCATT GTCAGGTTCT TCTCCCGGTT CACAGAGGTC
1141 AGGGAGTTTG CCATTGTTCC CCTGCATGCG GCGCCGGGGG ACGCAGTAGC CGAGATCGAC
1201 GCTCTCTATG ACGTCTACCT GGATGTCCAA GAGAAATGGG GCTTGGAGGA CGTCATGTTG
1261 ATGGGCGACT TCAATGCGGG CTGCAGCTAT GTGAGACCTT CCCAGTGGTC ATCCATCCGC
1321 CTGTGGACAA GCGCCACCTT CCAGTGGCTG ATCCCCGACA GCGCTGACAC CACAGCTACA
1381 CCCACGCACT GTGCCTATGA CAGGATCGTG GTTGCAAGGA TGCTGCTCCG AGGGGCGGTT
1441 GTTCCCGACT CGGCTCTTCC CTTTAACTTC CAGGCTGCCT ATGGCCTGAG TGACCAACTG
1501 GCCAAGCCA TCAGTGACCA CTATCCAGTG GAGGTGATGC TGAAGGGGGG CGGACCCAAA
1561 AAGAAGCGCA AGGTTTGA

```

//

└─→ NLS

**Fig. 17(A)**

LOCUS FDDNASE105 1578 BP SS-DNA SYN 25-AUG-2000

DEFINITION -

ACCESSION -

KEYWORDS -

SOURCE -

FEATURES Location/Qualifiers

frag join(1..>720,<781..1578)

frag 721..780

frag join(721..>735,<736..>759,<760..>780)

BASE COUNT 353 A 471 C 443 G 311 T 0 OTHER

ORIGIN -

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG

61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC

121 TGCAAGGCTT CTGGCTACAC CTTCACTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA

181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT

241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG

301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC

361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC

421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG

481 GCCCTGGGCT GCCTGGTCAA GGAAGTCTTC CCCGAACCGG TGACGGTGTC GTGGAAGTCA

541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCTTC AGGACTCTAC

601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC

661 AACGTGAATC ACAAGCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT

721 GACAAAACCTC ACACATGTCC ACCGTGTCCA GCACCAGAGG GCGGGCTGAA GATCGCAGCC

781 TTCAACATCC AGACATTTGG GGAGACCAAG ATGTCCAATG CCACCCTCGT CAGCTACATT

841 GTGCAGATCC TGAGCCGCTA CGACATCGCC CTGGTCCAGG AGGTCAGAGA CAGCCACCTG

901 ACTGCCGTGG GGAAGCTGCT GGACAACCTC AATCAGGACG CACCAGACAC CTATCACTAC

961 GTGGTCAGTG AGCCACTGGG ACGGAACAGC TATAAGGAGC GCTACCTGTT CGTGTACAGG

1021 CCTGACCAGG TGTCTGCGGT GGACAGCTAC TACTACGATG ATGGCTGCGA GCCCTGCGGG

1081 AACGACACCT TCAACCGAGA GCCAGCCATT GTCAGGTTCT TCTCCCGGTT CACAGAGGTC

1141 AGGGAGTTTG CCATTGTTCC CCTGCATGCG GCGCCGGGGG ACGCAGTAGC CGAGATCGAC

1201 GCTCTCTATG ACGTCTACCT GGATGTCCAA GAGAAATGGG GCTTGGAGGA CGTCATGTTG

1261 ATGGGCGACT TCAATGCGGG CTGCAGCTAT GTGAGACCCT CCCAGTGGTC ATCCATCCGC

1321 CTGTGGACAA GCGCCACCTT CCAGTGGCTG ATCCCCGACA GCGCTGACAC CACAGCTACA

1381 CCCACGCACT GTGCCTATGA CAGGATCGTG GTTGCAGGGA TGCTGCTCCG AGGGGCCGTT

1441 GTTCCCAGCT CGGCTCTTCC CTTTAACTTC CAGGCTGCCT ATGGCCTGAG TGACCAACTG

1501 GCCCAAGCCA TCAGTGACCA CTATCCAGTG GAGGTGATGC TGAAGGGGGG CGGACCCAAA

1561 AAGAAGCGCA AGGTTTGA

//

**Fig. 17(B)**

LOCUS FDDNASE105 1587 BP SS-DNA SYN 29-AUG-2000  
 DEFINITION -  
 ACCESSION -  
 KEYWORDS -  
 SOURCE -

FEATURES Location/Qualifiers  
 frag 10..1587  
 /note="1 to 1578 of FdDNase105correct"  
 frag join(10..>729,<790..1587)  
 /note="1 to 1578 of PAS105.dna [Split]"  
 frag 730..789  
 /note="1 to 60 of 101/105linker"  
 frag join(730..>744,<745..>768,<769..>789)  
 /note="1 to 80 of 102linker [Split]"

BASE COUNT 354 A 477 C 445 G 311 T 0 OTHER  
 ORIGIN -

```

1  GCGGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTGTC
61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG
121 AAGGTGTCCT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC
181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATTT TACCTGGAAG TAATAATTCT
241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA
361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA
421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCCT CCTCCAAGAG CACCTCTGGG
481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCCTG GACGGTGTCTG
541 TGGAACCTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCTT ACAGTCCTCA
601 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC
661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC
721 AAATCTTG TG ACAA AACTCA CACATGTCCA CCGTGTCCAG CACCAGAGGG CGGGCTGAAG
781 ATCGCAGCCT TCAACATCCA GACATTTGGG GAGACCAAGA TGTCCAATGC CACCCTCGTC
841 AGCTACATTG TGCAGATCCT GAGCCGCTAC GACATCGCCC TGGTCCAGGA GGTCAGAGAC
901 AGCCACCTGA CTGCCGTGGG GAAGCTGCTG GACAACCTCA ATCAGGACGC ACCAGACACC
961 TATCACTACG TGGTCAGTGA GCCACTGGGA CGGAACAGCT ATAAGGAGCG CTACCTGTTC
1021 GTGTACAGGC CTGACCAGGT GTCTGCGGTG GACAGCTACT ACTACGATGA TGGCTGCGAG
1081 CCCTGCGGGA ACGACACCTT CAACCGAGAG CCAGCCATTG TCAGGTTCTT CTCCCGGTTT
1141 ACAGAGGTCA GGGAGTTTGC CATTGTTCCC CTGCATGCGG CCCC GG GGA CGCAGTAGCC
1201 GAGATCGACG CTCTCTATGA CGTCTACCTG GATGTCCAAG AGAAATGGGG CTTGGAGGAC
1261 GTCATGTTGA TGGGCGACTT CAATGCGGGC TGCAGCTATG TGAGACCCTC CCAGTGGTCA
1321 TCCATCCGCC TGTGGACAAG CCCCACCTTC CAGTGGCTGA TCCCCGACAG CGCTGACACC
1381 ACAGCTACAC CCACGCACTG TGCCTATGAC AGGATCGTGG TTGCAGGGAT GCTGCTCCGA
1441 GGGGCCGTTG TTCCCGACTC GGCTCTTCCC TTAACTTCC AGGCTGCCTA TGGCCTGAGT
1501 GACCAACTGG CCAAGCCAT CAGTGACCAC TATCCAGTGG AGGTGATGCT GAAGGGGGGC
1561 GGACCCAAAA AGAAGCGCAA GGTTTGA

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**Fig. 17(C)**

```

          9          18          27          36          45          54
5'  ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC
    ---
    M  G  W  S  C  I  I  L  F  L  V  A  T  A  T  G  V  H

          63          72          81          90          99          108
TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA
    ---
    S  Q  V  Q  L  V  Q  S  G  A  E  V  K  K  P  G  A  S

          117          126          135          144          153          162
GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG
    ---
    V  K  V  S  C  K  A  S  G  Y  T  F  S  A  Y  W  I  E

          171          180          189          198          207          216
TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT
    ---
    W  V  R  Q  A  P  G  K  G  L  E  W  V  G  E  I  L  P

          225          234          243          252          261          270
GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT
    ---
    G  S  N  N  S  R  Y  N  E  K  F  K  G  R  V  T  V  T

          279          288          297          306          315          324
AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG
    ---
    R  D  T  S  T  N  T  A  Y  M  E  L  S  S  L  R  S  E

          333          342          351          360          369          378
GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC
    ---
    D  T  A  V  Y  Y  C  A  R  S  Y  D  F  A  W  F  A  Y

          387          396          405          414          423          432
TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG
    ---
    W  G  Q  G  T  L  V  T  V  S  S  A  S  T  K  G  P  S

          441          450          459          468          477          486
GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG
    ---
    V  F  P  L  A  P  S  S  K  S  T  S  G  G  T  A  A  L

          495          504          513          522          531          540
GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA
    ---
    G  C  L  V  K  D  Y  F  P  E  P  V  T  V  S  W  N  S

          549          558          567          576          585          594
GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA
    ---
    G  A  L  T  S  G  V  H  T  F  P  A  V  L  Q  S  S  G

```

**Fig. 17(D)**  
(Sheet 1 of 3)



GCC	GAG	ATC	GAC	GCT	CTC	TAT	GAC	GTC	TAC	CTG	GAT	GTC	CAA	GAG	AAA	TGG	GGC	
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
A	E	I	D	A	L	Y	D	V	Y	L	D	V	Q	E	K	W	G	
1251				1260			1269			1278			1287			1296		
TTG	GAG	GAC	GTC	ATG	TTG	ATG	GGC	GAC	TTC	AAT	GCG	GGC	TGC	AGC	TAT	GTG	AGA	
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
L	E	D	V	M	L	M	G	D	F	N	A	G	C	S	Y	V	R	
1305				1314			1323			1332			1341			1350		
CCC	TCC	CAG	TGG	TCA	TCC	ATC	CGC	CTG	TGG	ACA	AGC	CCC	ACC	TTC	CAG	TGG	CTG	
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
P	S	Q	W	S	S	I	R	L	W	T	S	P	T	F	Q	W	L	
1359				1368			1377			1386			1395			1404		
ATC	CCC	GAC	AGC	GCT	GAC	ACC	ACA	GCT	ACA	CCC	ACG	CAC	TGT	GCC	TAT	GAC	AGG	
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
I	P	D	S	A	D	T	T	A	T	P	T	H	C	A	Y	D	R	
1413				1422			1431			1440			1449			1458		
ATC	GTG	GTT	GCA	GGG	ATG	CTG	CTC	CGA	GGG	GCC	GTT	GTT	CCC	GAC	TCG	GCT	CTT	
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
I	V	V	A	G	M	L	L	R	G	A	V	V	P	D	S	A	L	
1467				1476			1485			1494			1503			1512		
CCC	TTT	AAC	TTC	CAG	GCT	GCC	TAT	GGC	CTG	AGT	GAC	CAA	CTG	GCC	CAA	GCC	ATC	
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
P	F	N	F	Q	A	A	Y	G	L	S	D	Q	L	A	Q	A	I	
1521				1530			1539			1548			1557			1566		
AGT	GAC	CAC	TAT	CCA	GTG	GAG	GTG	ATG	CTG	AAG	GGG	GGC	GGA	CCC	AAA	AAG	AAG	
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
S	D	H	Y	P	V	E	V	M	L	K	G	G	G	P	K	K	K	
1575																		
CGC	AAG	GTT	TGA	3'														
---	---	---	---															
R	K	V	*															

**Fig. 17(D)**  
(Sheet 3 of 3)



## pAS106

LOCUS PAS106.DNA 1596 bp mRNA PRI 06-MAR-1995  
DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I with SV40  
NLS (pAS106)  
ACCESSION  
NID  
KEYWORDS DNase I.  
SOURCE DNase I sequence is from assembled oligos (thus modified c/f  
MHDNASE1.dna)  
ORGANISM Homo sapiens  
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;  
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.  
TITLE Recombinant human DNase I reduces the viscosity of cystic  
fibrosis  
sputum  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)  
MEDLINE 91067672  
BASE COUNT 355 a 475 c 452 g 314 t  
ORIGIN

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1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCACTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACCTCA
541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAACTC ACACATGCTG TGTGGAGTGC CCACCGTGCC CAGCACCTGA AGGGAGCGGC
781 GGGCTGAAGA TCGCAGCCTT CAACATCCAG ACATTTGGGG AGACCAAGAT GTCCAATGCC
841 ACCCTCGTCA GCTACATTGT GCAGATCCTG AGCCGCTACG ACATCGCCCT GGTCCAGGAG
901 GTCAGAGACA GCCACCTGAC TGCCGTGGGG AAGCTGCTGG ACAACCTCAA TCAGGACGCA
961 CCAGACACCT ATCACTACGT GGTCACTGAG CCACTGGGAC GGAACAGCTA TAAGGAGCGC
1021 TACCTGTTTC TGTACAGGCC TGACCAGGTG TCTGCGGTGG ACAGCTACTA CTACGATGAT
1081 GGCTGCGAGC CCTGCGGGAA CGACACCTTC AACCGAGAGC CAGCCATTGT CAGGTTCTTC
1141 TCCCGGTTCA CAGAGGTCAG GGAGTTTGCC ATTGTTCCCC TGCATGCGGC CCCGGGGGAC
1201 GCAGTAGCCG AGATCGACGC TCTCTATGAC GTCTACCTGG ATGTCCAAGA GAAATGGGGC
1261 TTGGAGGACG TCATGTTGAT GGGCGACTTC AATGCGGGCT GCAGCTATGT GAGACCCTCC
1321 CAGTGGTCAT CCATCCGCCT GTGGACAAGC CCCACCTTCC AGTGGCTGAT CCCCACAGC
1381 GCTGACACCA CAGCTACACC CACGCACTGT GCCTATGACA GGATCGTGGT TGCAGGGATG
1441 CTGCTCCGAG GGGCCGTTGT TCCGACTCG GCTCTTCCCT TTAACCTCCA GGCTGCCTAT
1501 GGCCTGAGTG ACCAACTGGC CCAAGCCATC AGTGACCACT ATCCAGTGA GGTGATGCTG
1561 AAGGGGGGCG GACCCAAAA GAAGCGCAAG GTTTGA
```

//

→ NLS

**Fig. 18(A)**

LOCUS FDDNASE106 1596 BP SS-DNA SYN 25-AUG-2000

DEFINITION -

ACCESSION -

KEYWORDS -

SOURCE -

FEATURES Location/Qualifiers

frag join(1..>720,<799..1596)

frag /note="1 to 1596 of PAS106.dna [Split]"

frag 721..798

/note="1 to 78 of 102/106linker"

BASE COUNT 355 A 474 C 452 G 315 T 0 OTHER

ORIGIN -

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG

61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC

121 TGCAAGGCTT CTGGCTACAC CTTCAAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA

181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT

241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG

301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC

361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC

421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG

481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGGTGC GTGGAACCTA

541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC

601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC

661 AACGTGAATC ACAAGCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT

721 GACAAACTC ACACATGCTG TGTCGAGTGT CCACCGTGTC CAGCACCAGA GGGGAGCGGC

781 GGGCTGAAGA TCGCAGCCTT CAACATCCAG ACATTTGGGG AGACCAAGAT GTCCAATGCC

841 ACCCTCGTCA GCTACATTGT GCAGATCCTG AGCCGCTACG ACATCGCCCT GGTCCAGGAG

901 GTCAGAGACA GCCACCTGAC TGCCGTGGGG AAGCTGCTGG ACAACCTCAA TCAGGACGCA

961 CCAGACACCT ATCACTACGT GGTCACTGAG CCACTGGGAC GGAACAGCTA TAAGGAGCGC

1021 TACCTGTTTG TGTACAGGCC TGACCAGGTG TCTGCGGTGG ACAGCTACTA CTACGATGAT

1081 GGCTGCGAGC CCTGCGGGAA CGACACCTTC AACCAGAGAG CAGCCATTGT CAGGTTCTTC

1141 TCCCGGTTCA CAGAGGTCAG GGAGTTTGCC ATTGTTCCCC TGCATGCGGC CCCGGGGGAC

1201 GCAGTAGCCG AGATCGACGC TCTCTATGAC GTCTACCTGG ATGTCCAAGA GAAATGGGGC

1261 TTGGAGGACG TCATGTTGAT GGGCGACTTC AATGCGGGCT GCAGCTATGT GAGACCTCC

1321 CAGTGGTCAT CCATCCGCCT GTGGACAAGC CCCACCTTCC AGTGGCTGAT CCCCAGACAGC

1381 GCTGACACCA CAGCTACACC CACGCACTGT GCCTATGACA GGATCGTGGT TGCAGGGATG

1441 CTGCTCCGAG GGGCCGTTGT TCCCGACTCG GCTCTTCCCT TTAACCTCCA GGCTGCCTAT

1501 GGCCTGAGTG ACCAAGTGG CCAAGCCATC AGTGACCACT ATCCAGTGGA GGTGATGCTG

1561 AAGGGGGGCG GACCCAAAAA GAAGCGCAAG GTTTGA

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**Fig. 18(B)**

LOCUS FDDNASE106 1605 BP SS-DNA SYN 29-AUG-2000  
 DEFINITION -  
 ACCESSION -  
 KEYWORDS -  
 SOURCE -

FEATURES Location/Qualifiers  
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 frag join(10..>729,<808..1605)  
 /note="1 to 1596 of PAS106.dna [Split]"  
 frag 730..807  
 /note="1 to 78 of 102/106linker"

BASE COUNT 356 A 480 C 454 G 315 T 0 OTHER  
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181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATTT TACCTGGAAG TAATAATTCT
241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA
361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA
421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCT CCTCCAAGAG CACCTCTGGG
481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTCTG
541 TGGAACTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCTT ACAGTCCTCA
601 GGA CTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC
661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC
721 AAATCTTGTG ACAAACCTCA CACATGCTGT GTCGAGTGTC CACCGTGTCC AGCACCAGAG
781 GGGAGCGGCG GGCTGAAGAT CGCAGCCTTC AACATCCAGA CATTTGGGGA GACCAAGATG
841 TCCAATGCCA CCCTCGTCAG CTACATTGTG CAGATCCTGA GCCGCTACGA CATCGCCCTG
901 GTCCAGGAGG TCAGAGACAG CCACCTGACT GCCGTGGGGA AGCTGCTGGA CAACCTCAAT
961 CAGGACGCAC CAGACACCTA TCACTACGTG GTCAGTGAGC CACTGGGACG GAACAGCTAT
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1141 AGGTTCTTCT CCCGTTTAC AGAGGTCAGG GAGTTTGCCA TTGTTCCCTT GCATGCGGCC
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1381 CCCGACAGCG CTGACACCAC AGCTACACCC ACGCACTGTG CCTATGACAG GATCGTGGTT
1441 GCAGGGATGC TGCTCCGAGG GGCCGTTGTT CCCGACTCGG CTCTTCCCTT TAACCTCCAG
1501 GCTGCCTATG GCCTGAGTGA CCAACTGGCC CAAGCCATCA GTGACCACTA TCCAGTGGAG
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**Fig. 18(C)**







## pAS107

LOCUS PAS107.DNA 1590 bp mRNA PRI 06-MAR-1995  
 DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I with SV40  
 NLS(pAS107)  
 ACCESSION  
 NID  
 KEYWORDS DNase I.  
 SOURCE DNase I sequence is from assembled oligos (thus modified c/f  
 MHDNASE1.dna)  
 ORGANISM Homo sapiens  
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;  
 Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 AUTHORS Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.  
 TITLE Recombinant human DNase I reduces the viscosity of cystic  
 fibrosis  
 sputum  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)  
 MEDLINE 91067672  
 BASE COUNT 354 a 474 c 448 g 314 t  
 ORIGIN

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181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
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1201 GCCGAGATCG ACGCTCTCTA TGACGTCTAC CTGGATGTCC AAGAGAAATG GGGCTTGGAG
1261 GACGTCATGT TGATGGGCGA CTTCAATGCG GGCTGCAGCT ATGTGAGACC CTCCCAGTGG
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1381 ACCACAGCTA CACCCACGCA CTGTGCCTAT GACAGGATCG TGTTGTCAGG GATGCTGCTC
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└─ NLS

**Fig. 19(A)**

LOCUS FDDNASE107 1590 BP SS-DNA SYN 25-AUG-2000  
 DEFINITION -  
 ACCESSION -  
 KEYWORDS -  
 SOURCE -

FEATURES Location/Qualifiers  
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 frag 721..792  
 /note="1 to 72 of 103/107linker"  
 frag join(721..>771,<772..792)  
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BASE COUNT 354 A 473 C 448 G 315 T 0 OTHER

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 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC  
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**Fig. 19(B)**



LOCUS FDDNASE107 1599 BP SS-DNA SYN 29-AUG-2000  
 DEFINITION -  
 ACCESSION -  
 KEYWORDS -  
 SOURCE -

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 frag join(10..>729,<802..1599)  
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 frag 730..801  
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BASE COUNT 355 A 479 C 450 G 315 T 0 OTHER

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 301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA  
 361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA  
 421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCCT CCTCCAAGAG CACCTCTGGG  
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 961 GCACCAGACA CCTATCACTA CGTGGTCAGT GAGCCACTGG GACGGAACAG CTATAAGGAG  
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 1261 GGCTTGGAGG ACGTCATGTT GATGGGCGAC TTCAATGCGG GCTGCAGCTA TGTGAGACCC  
 1321 TCCCAGTGTT CATCCATCCG CCTGTGGACA AGCCCCACCT TCCAGTGGCT GATCCCCGAC  
 1381 AGCGCTGACA CCACAGCTAC ACCCACGCAC TGTGCCTATG ACAGGATCGT GGTGTCAGGG  
 1441 ATGCTGCTCC GAGGGGCGGT TGTTCCTGAC TCGGCTCTTC CTTTAACTT CCAGGCTGCC  
 1501 TATGGCCTGA GTGACCAACT GGCCCAAGCC ATCAGTGACC ACTATCCAGT GGAGGTGATG  
 1561 CTGAAGGGGG GCGGACCCAA AAAGAAGCGC AAGGTTTGA

//

**Fig. 19(C)**

5' ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC  
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 M G W S C I I L F L V A T A T G V H

63 72 81 90 99 108  
 TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA  
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 S Q V Q L V Q S G A E V K K P G A S

117 126 135 144 153 162  
 GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG  
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 V K V S C K A S G Y T F S A Y W I E

171 180 189 198 207 216  
 TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT  
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 W V R Q A P G K G L E W V G E I L P

225 234 243 252 261 270  
 GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT  
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 G S N N S R Y N E K F K G R V T V T

279 288 297 306 315 324  
 AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG  
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 R D T S T N T A Y M E L S S L R S E

333 342 351 360 369 378  
 GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC  
 ---  
 D T A V Y Y C A R S Y D F A W F A Y

387 396 405 414 423 432  
 TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG  
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 W G Q G T L V T V S S A S T K G P S

441 450 459 468 477 486  
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495 504 513 522 531 540  
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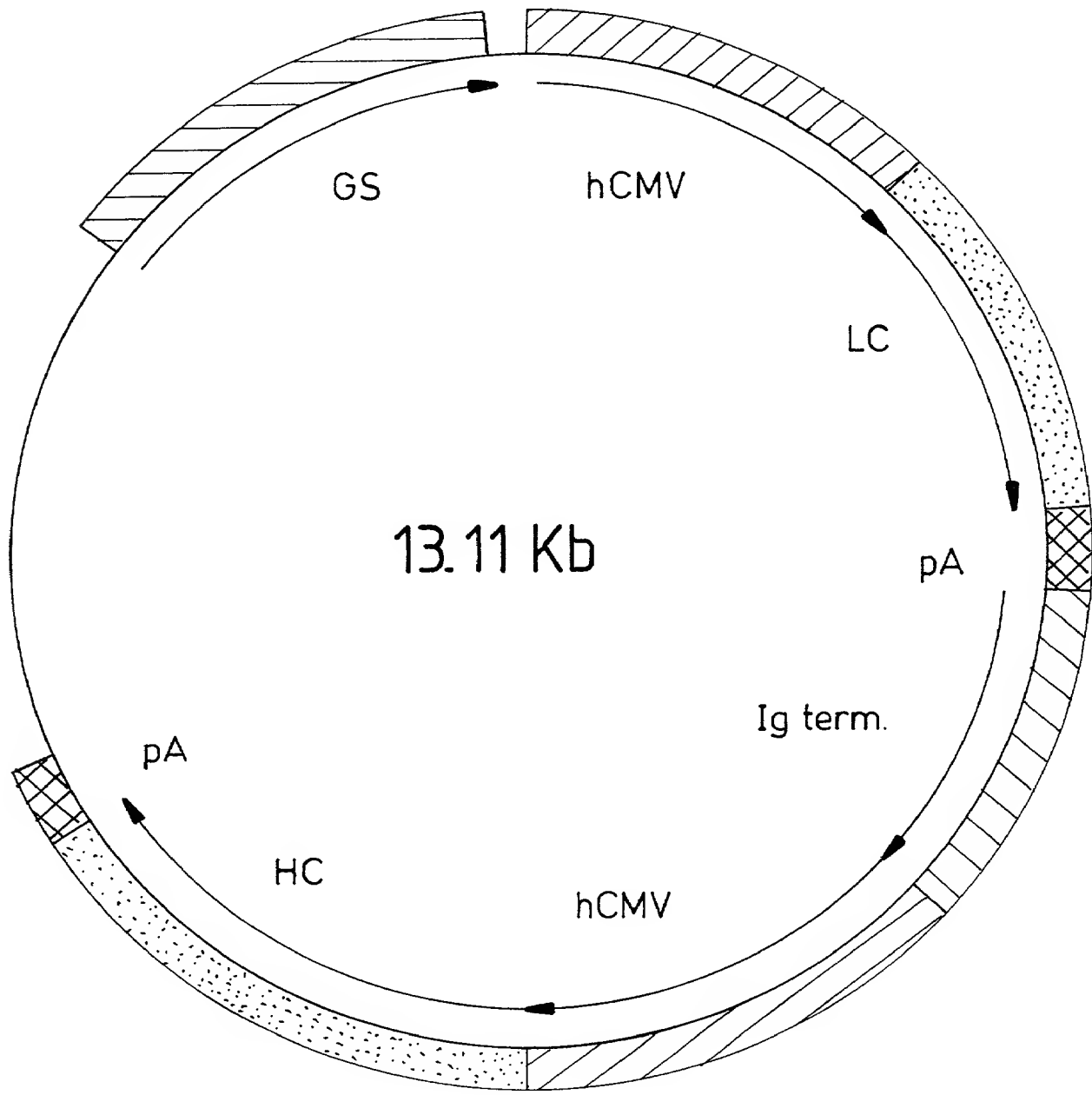
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**Fig. 19(D)**  
**(Sheet 1 of 3)**



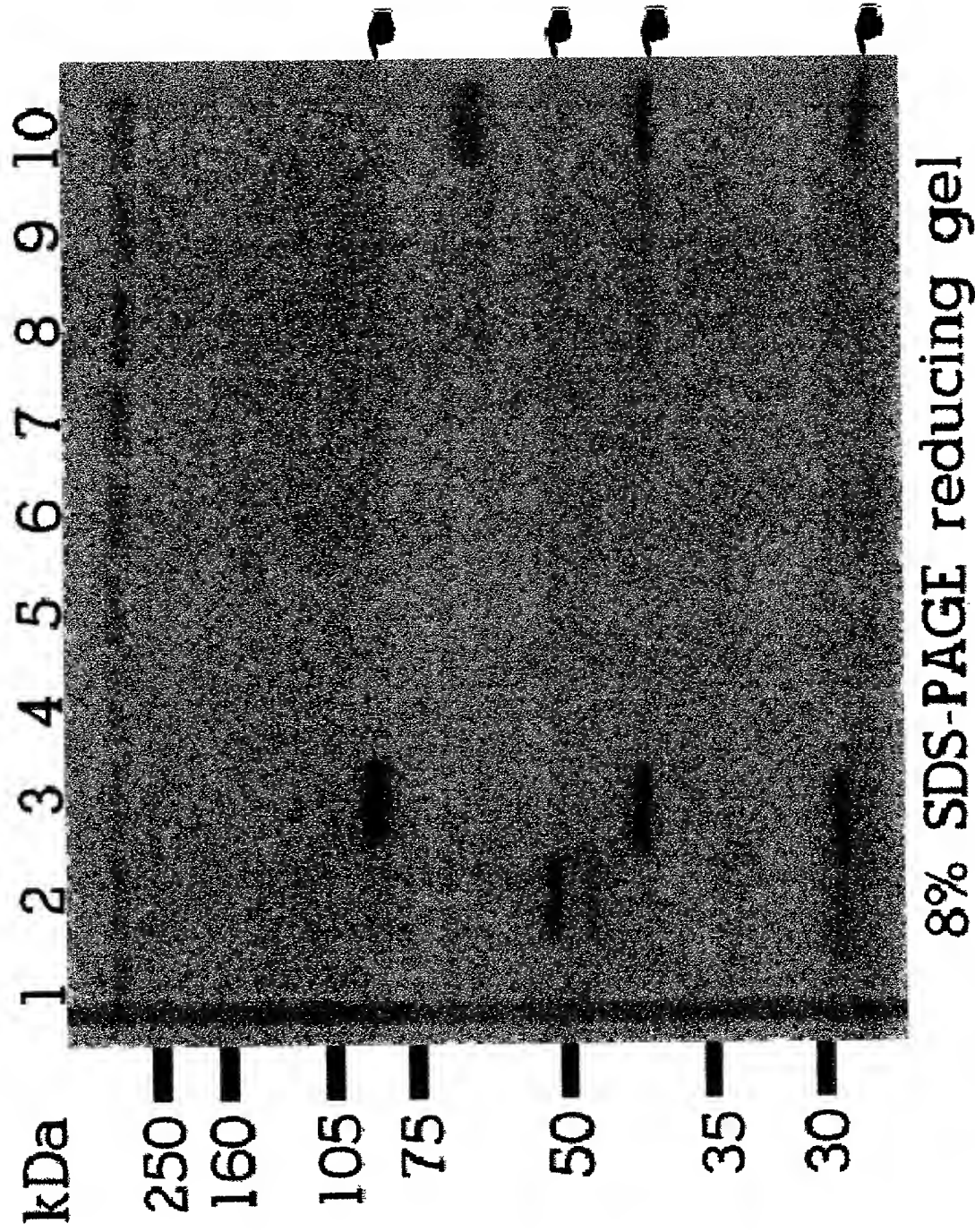


Mammalian expression of humanised HMFG1-D Nase constructs



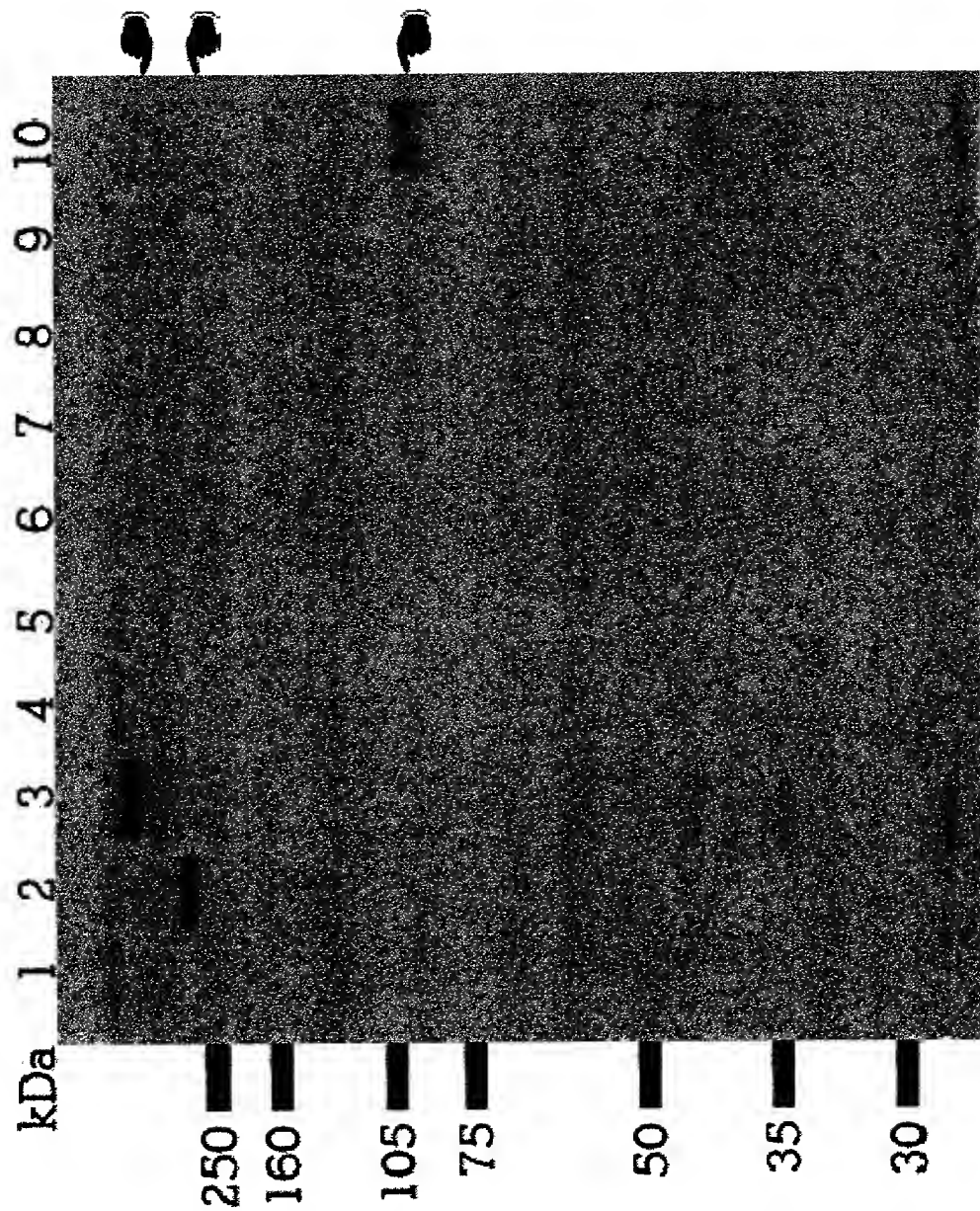
*Fig. 20*

Immuno-precipitation of metabolically labelled transient transfectants



**Fig. 21(A)**

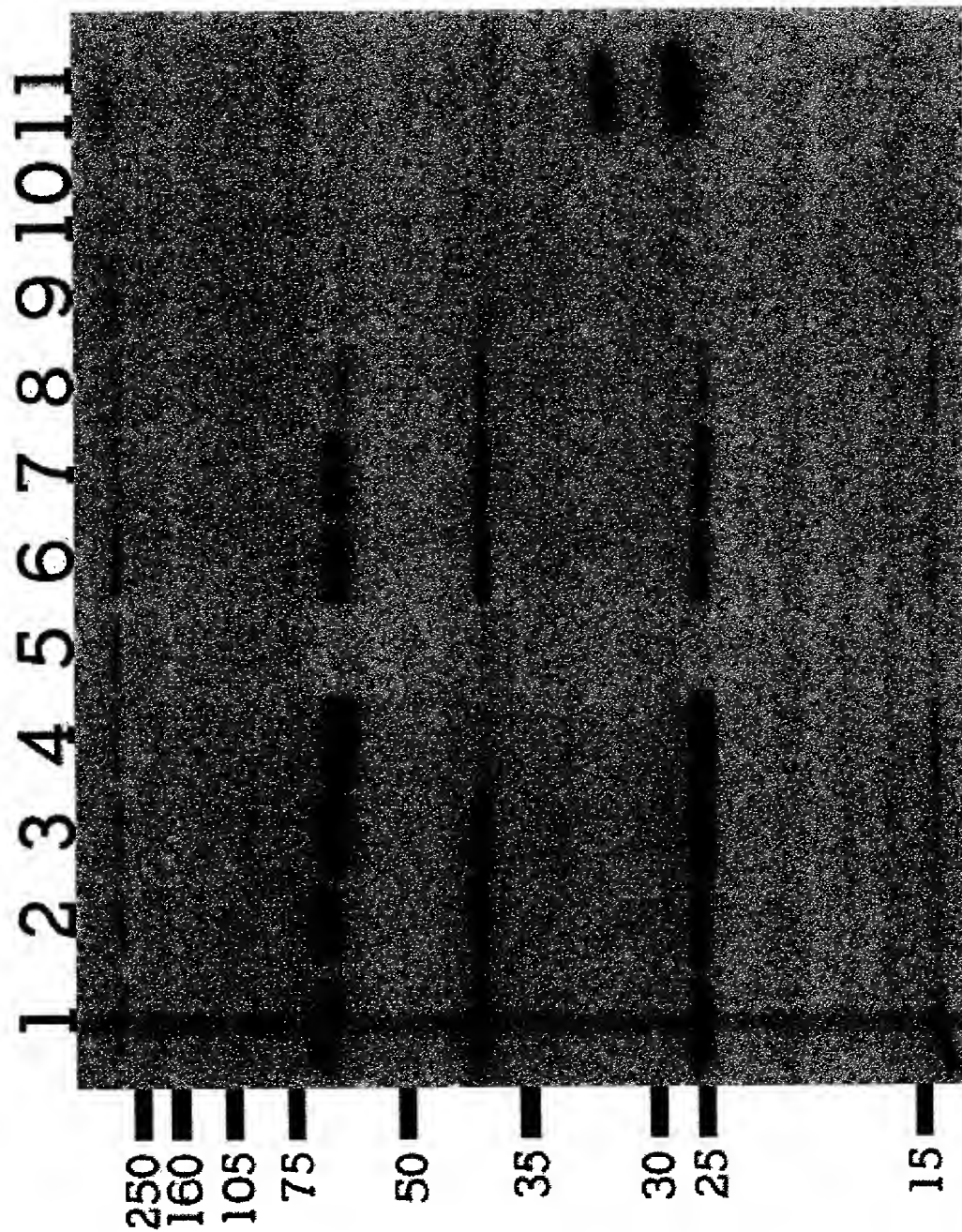
Immunoprecipitation of metabolically labelled transient transfectants



8% SDS-PAGE non-reducing gel

**Fig. 21(B)**

Immuno-precipitation of metabolically labelled transient transfectants

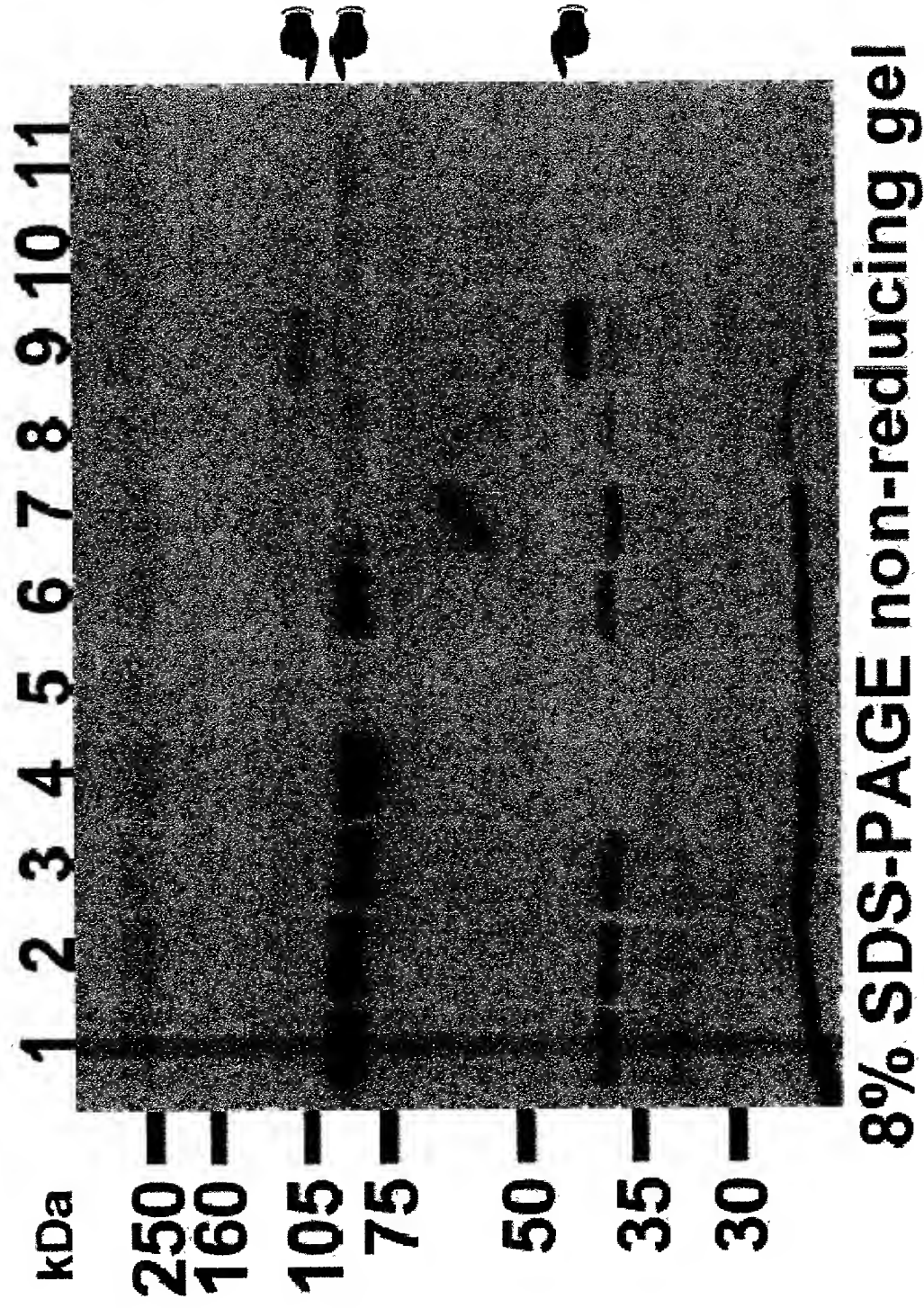


10% SDS-PAGE reducing gel

**Fig. 21(C)**



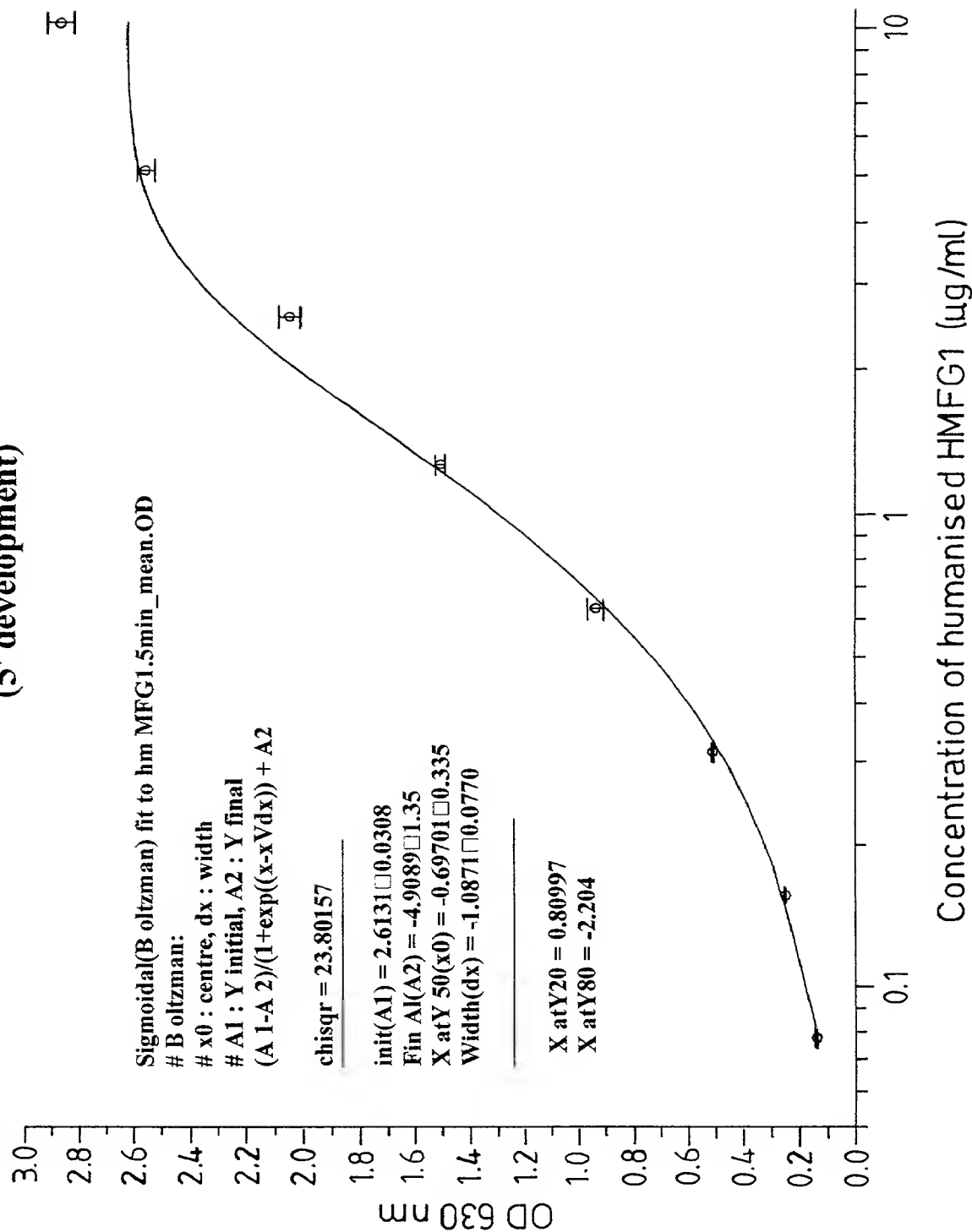
Immuno-precipitation of metabolically labelled transient transfectants



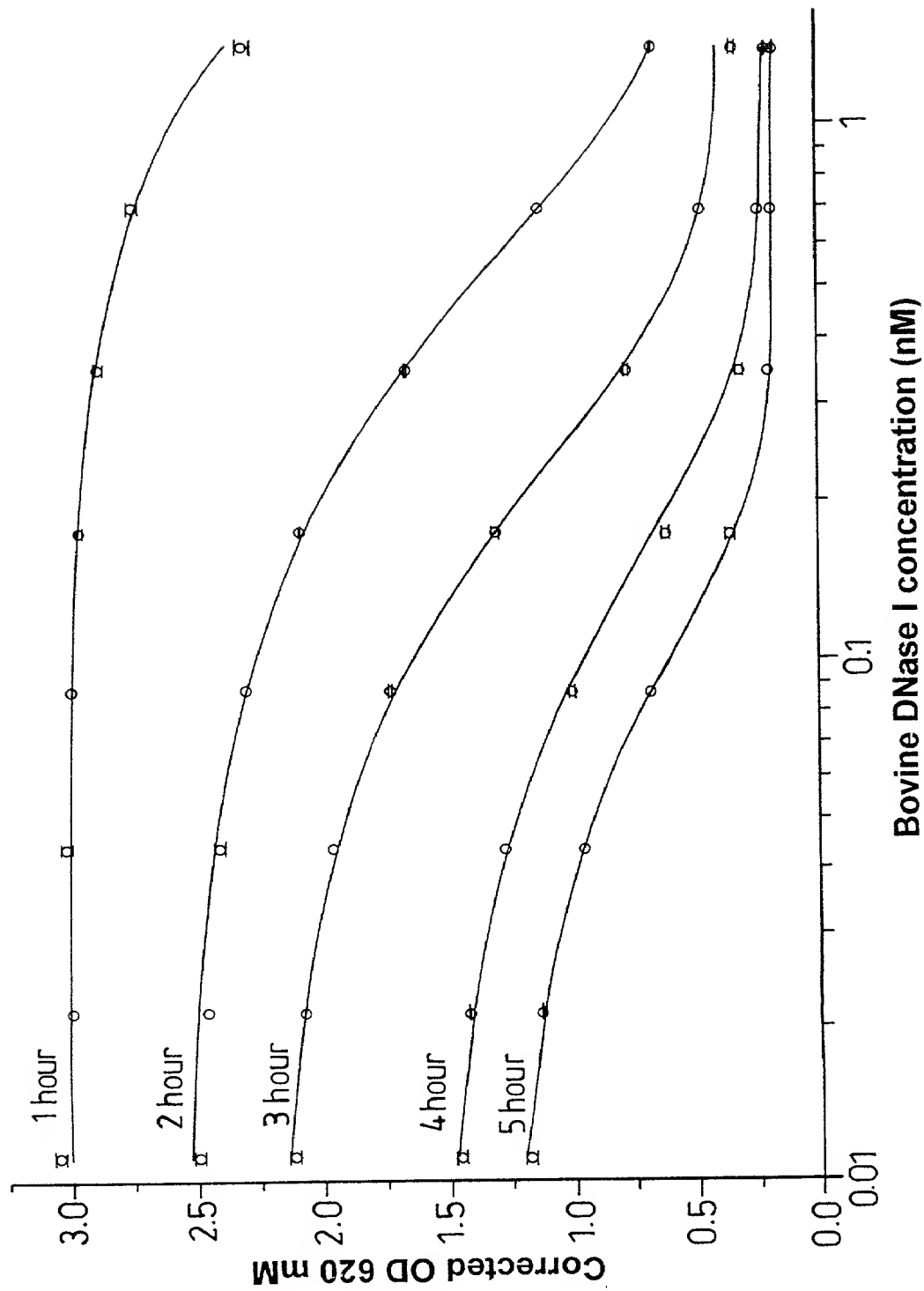
*Fig. 21(D)*

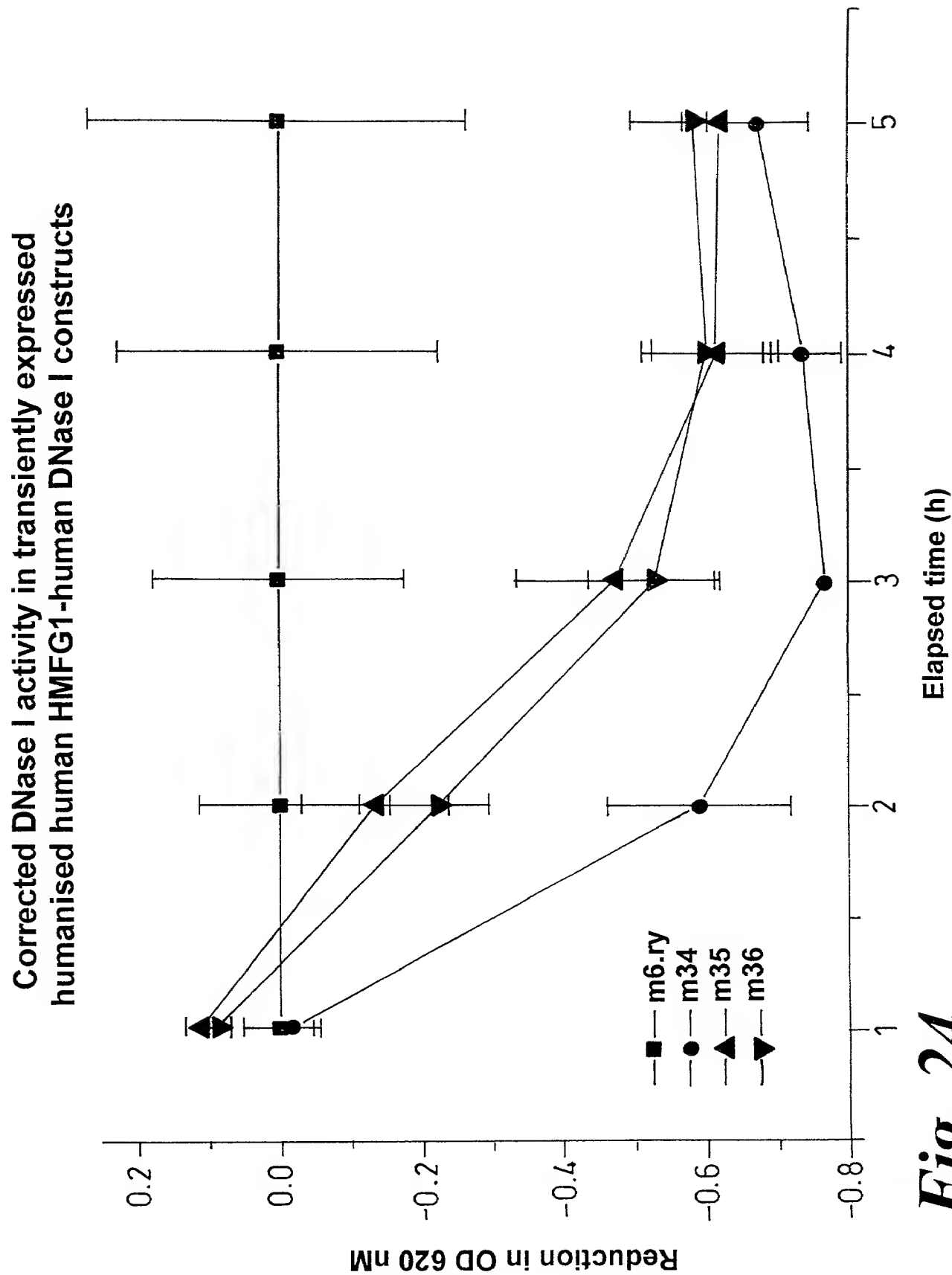
**Fig. 22**

PDTRP binding assay standard curve  
(5' development)



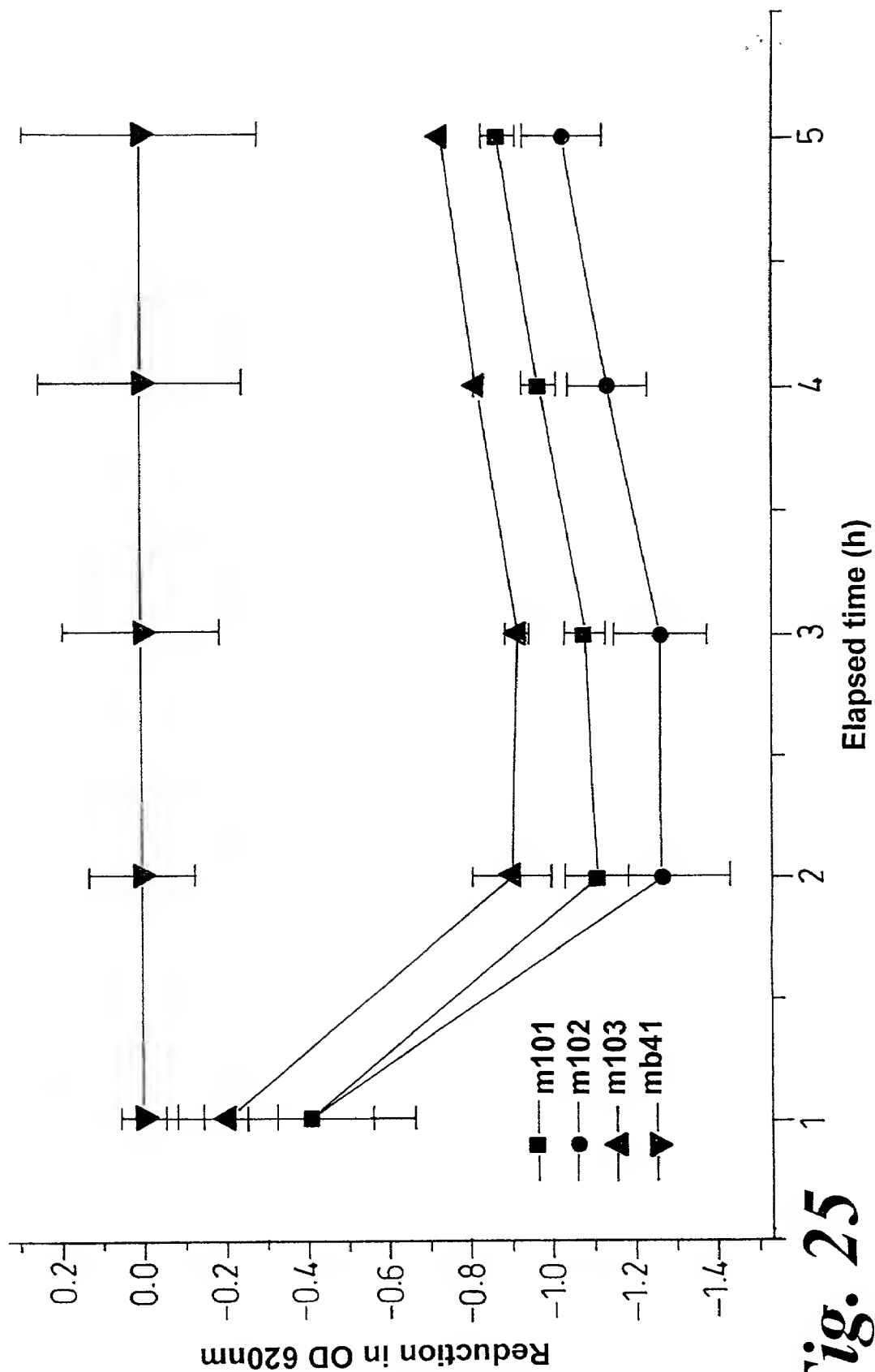
**Fig. 23** Corrected bovine DNase I standard curves at various time points





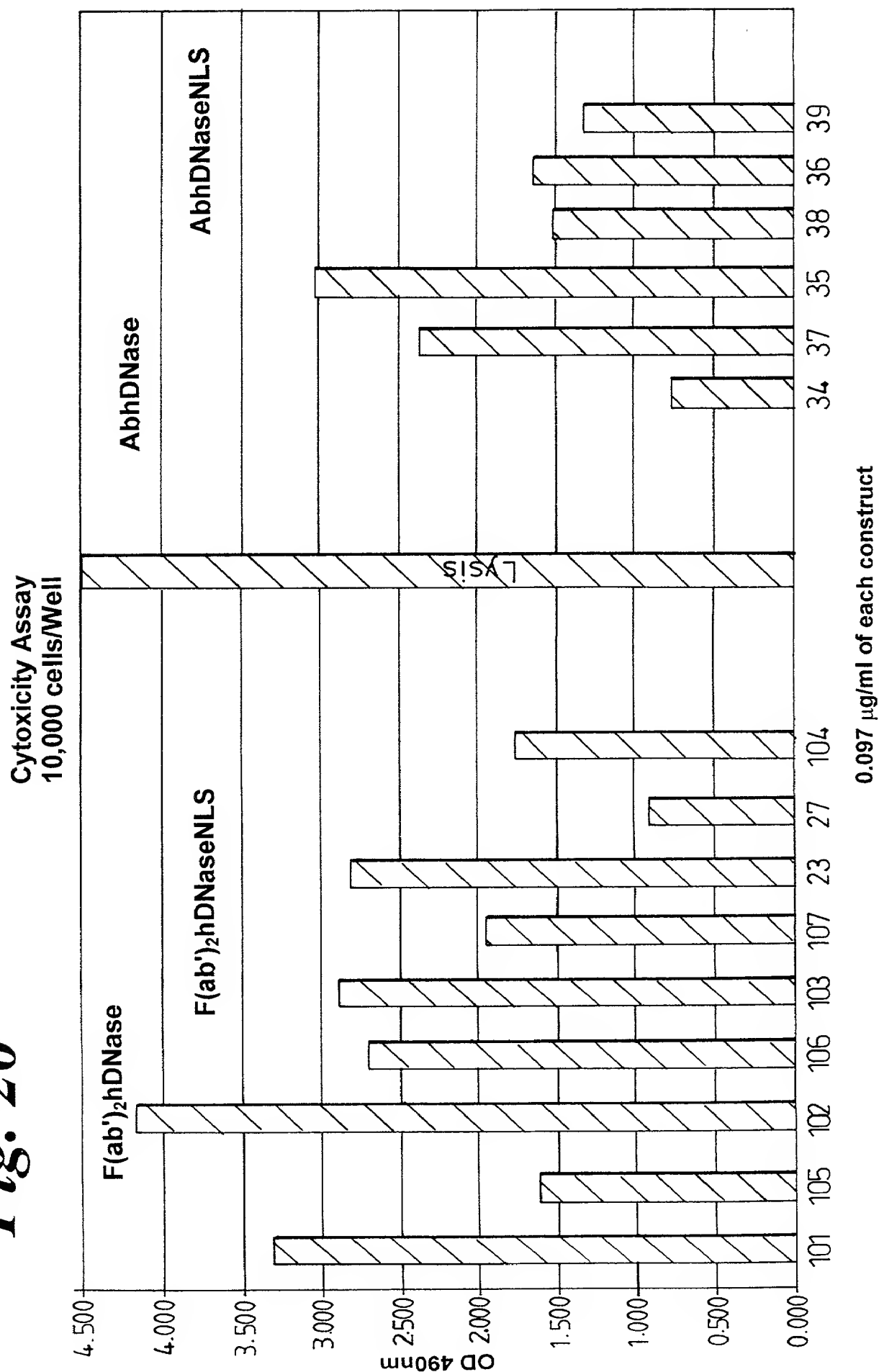
**Fig. 24**

Corrected DNase I activity in transiently expressed  
humanised HMFG1 F(ab')<sub>2</sub>-human DNase I fusions



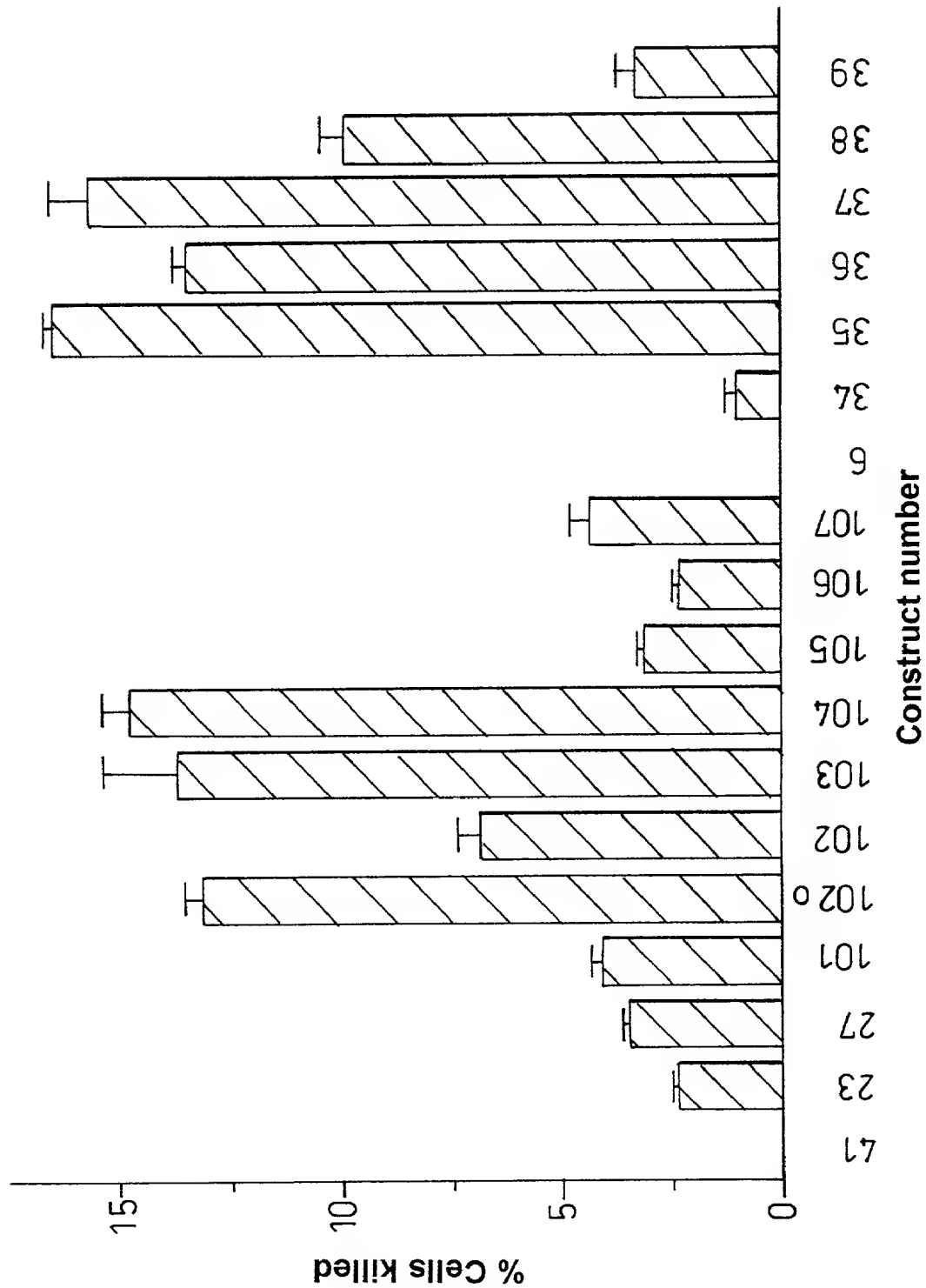
**Fig. 25**

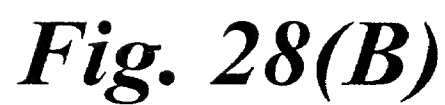
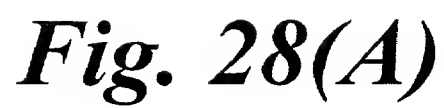
**Fig. 26**



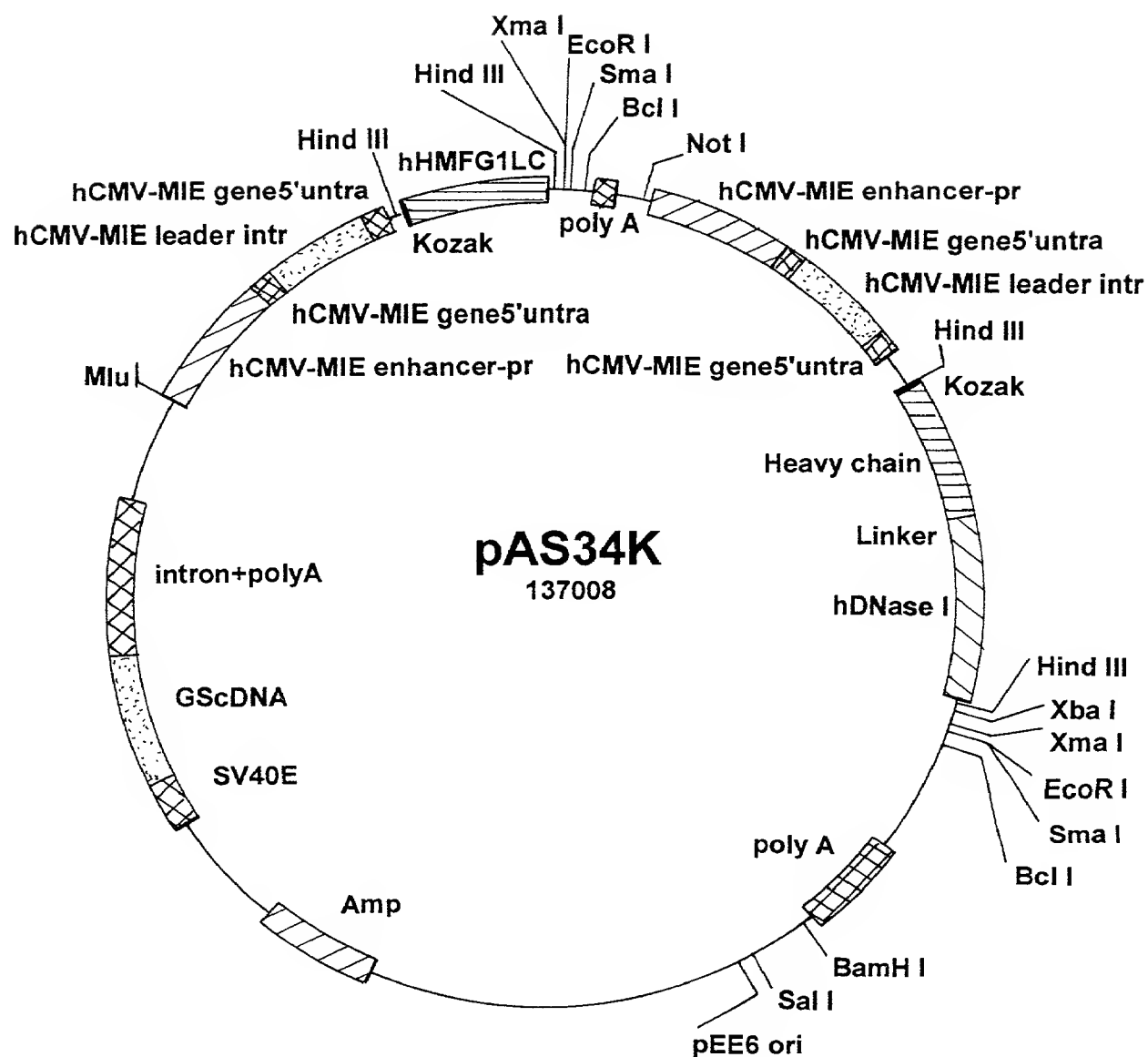
**Fig. 27**

MCF7 cells killed after 1h incubation with 1.35 ng of sample





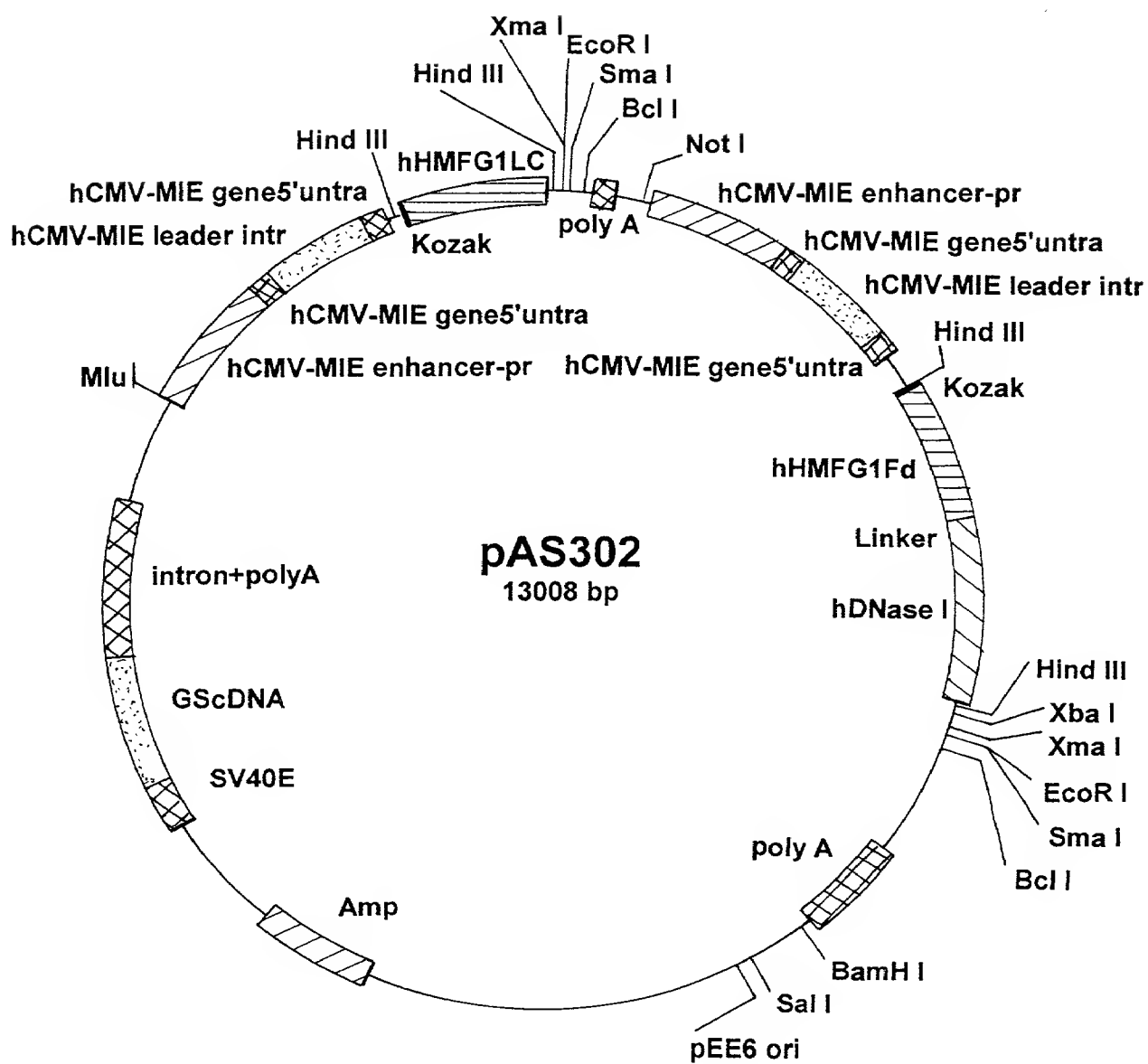




**Ab-DNase**

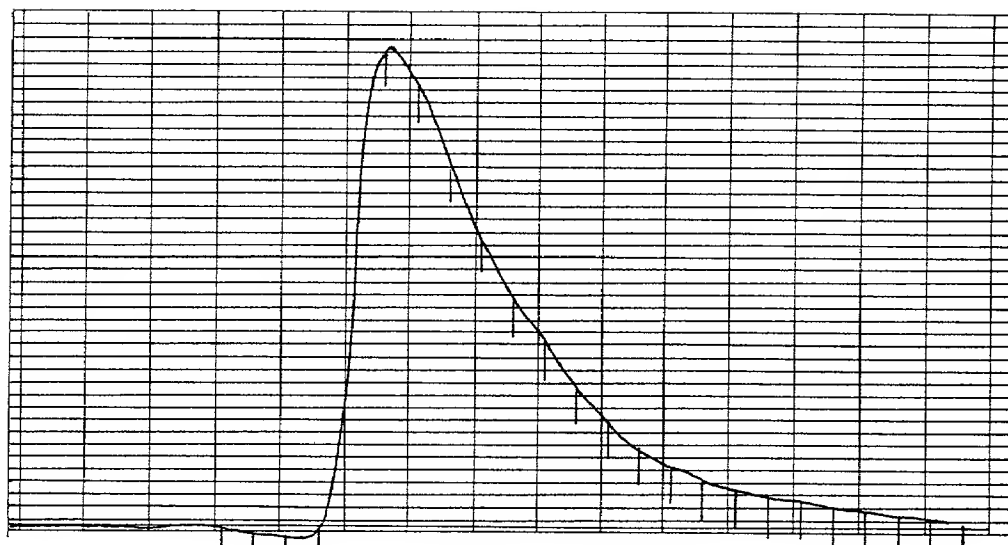
***Fig. 29***

700T60-27030360

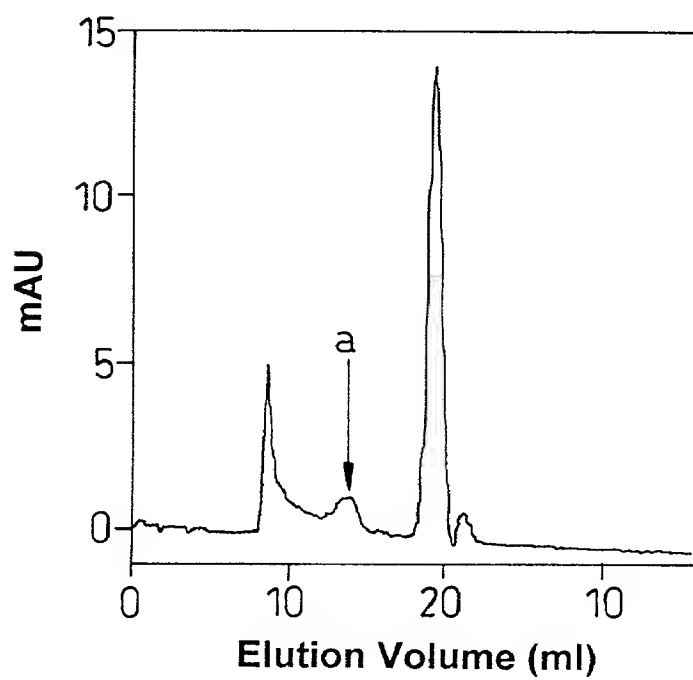


**Fab-DNase**

*Fig. 30*



***Fig. 31(A)***

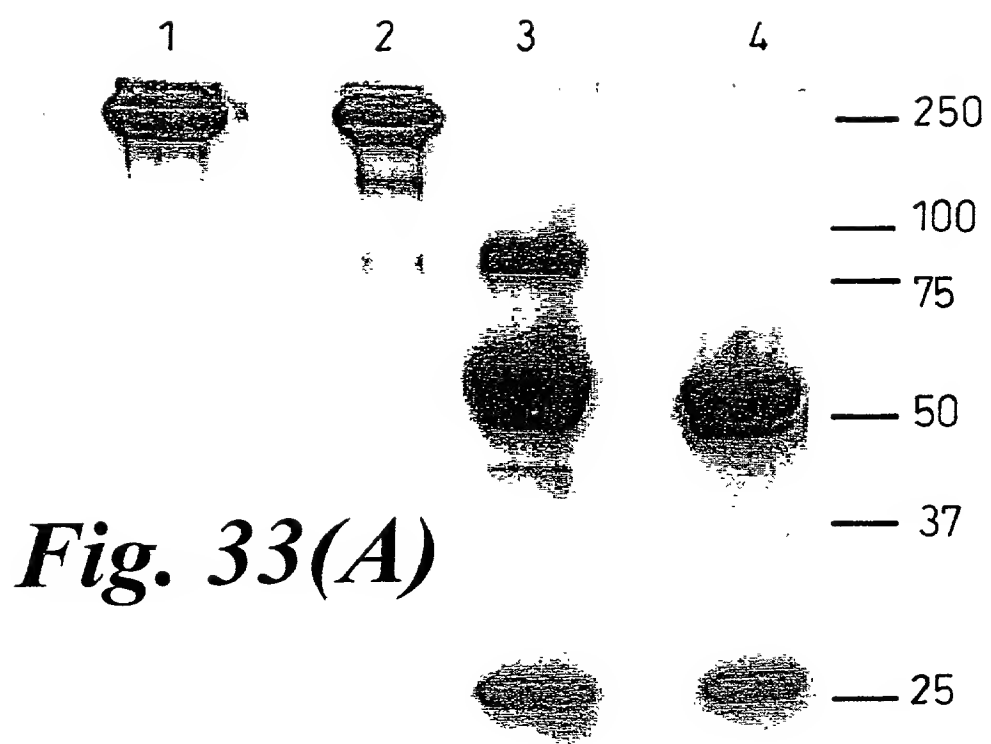


***Fig. 31(B)***

A chromatogram plot with 'mAU' on the y-axis (0 to 8) and 'Elution Volume (ml)' on the x-axis (0 to 35). A single, sharp, prominent peak is visible at approximately 12.5 ml, reaching a height of about 7 mAU. The baseline is stable and near zero throughout the rest of the run.

***Fig. 32(B)***

Fig. 33(A)

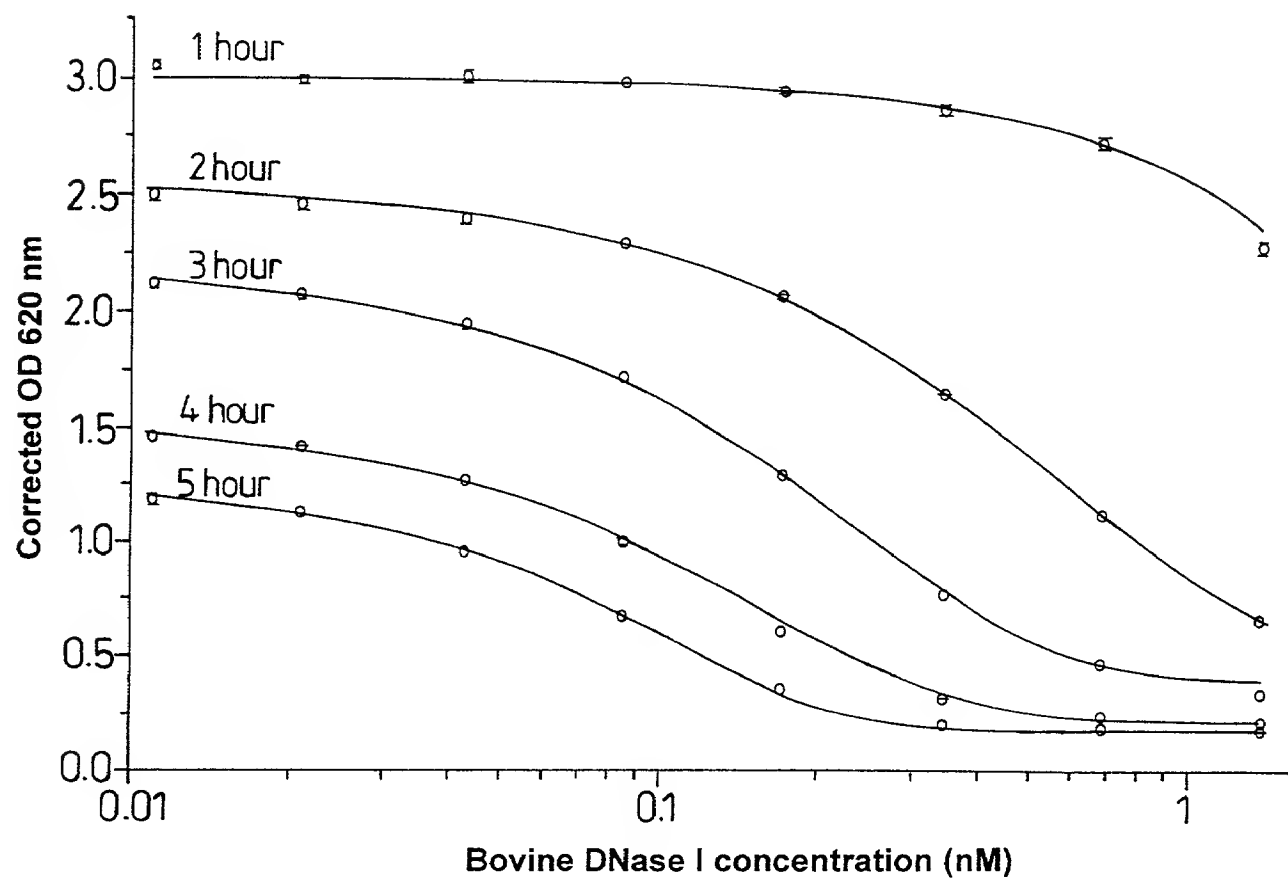


*Fig. 33(A)*



*Fig. 33(B)*

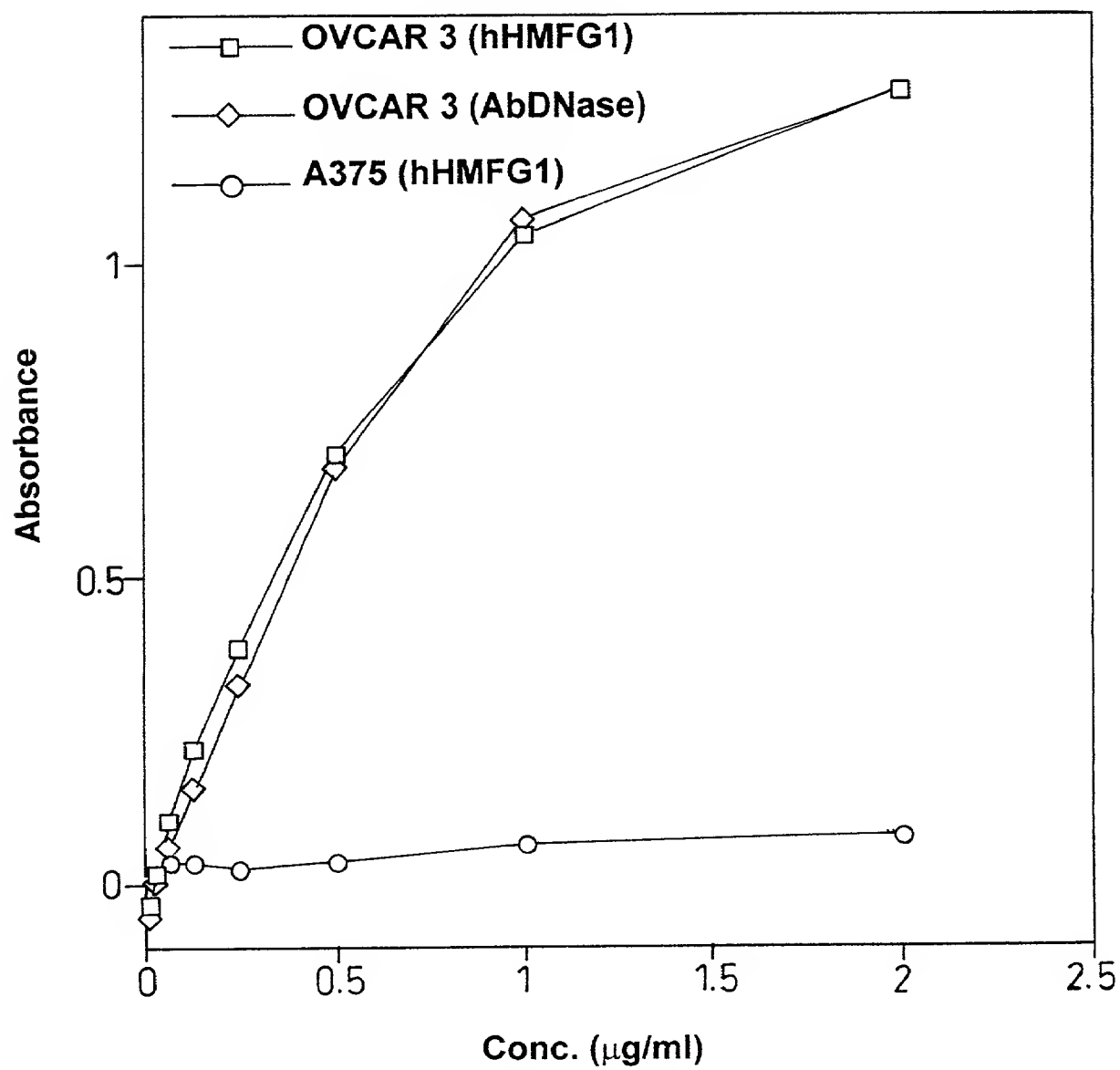
### Bovine DNase I standard curves at various time points



***Fig. 34(A)***

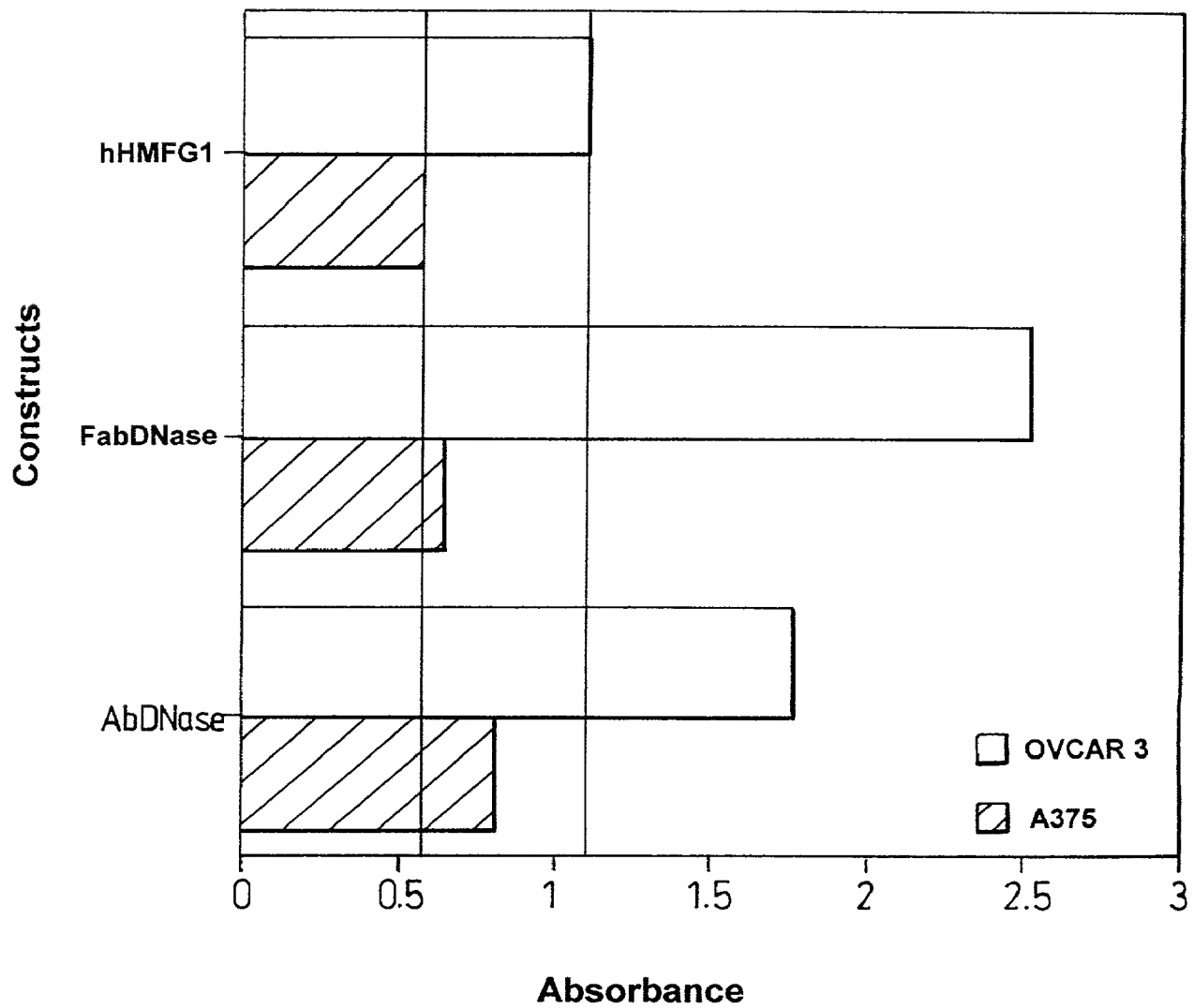
Constructs	3 hour	6 hour
Fab	~2.2	~1.7
bDNase (25ng)	~0.25	~0.2
AbDNase	~0.25	~0.2
FabDNase	~0.25	~0.15

***Fig. 34(B)***



***Fig. 35(A)***





***Fig. 35(B)***